

GenCore version 4.5
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OM protein - protein search, using SW model

Run on: August 12, 2002, 09:04:28 ; Search time 24.34 Seconds

(without alignments)
1420.565 Million cell updates/sec

Title: 09-09-707-121-2
Perfect score: 4721
Sequence: 1 MFPLKDAEMGAFEFASALP.....DGGINKIKPGLITIPSPQI 893

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 48719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_40*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	DB ID	Description
1	286.5	6.1	611	1	SNF1_CANCA	Q00372 candida gla
2	282	6.0	619	1	SNF1_CANTR	Q94168 candida tro
3	280	5.9	1142	1	GIN4_YEAST	Q12263 saccharomyc
4	275	5.8	576	1	SNF1_SCHPO	Q74536 schizosacch
5	274	5.8	620	1	SNF1_CANAL	P52497 candida alb
6	268	5.7	633	1	SNF1_YEAST	P06782 saccharomyc
7	266.5	5.6	326	1	CKK6_HUMAN	Q00534 homo sapien
8	260.5	5.5	547	1	SPAK_HUMAN	Q94968 homo sapien
9	257	5.4	615	1	CKK_RAT	Q09011 rattus norv
10	252	5.3	512	1	K110_ARATH	Q48997 arabidopsis
11	252	5.3	705	1	CC5_YEAST	P32562 saccharomyc
12	251.5	5.3	631	1	CKK_MOUSE	Q06806 mus musculu
13	250	5.3	553	1	SPAK_RAT	P08508 rattus norv
14	249	5.3	683	1	PLD1_SCHPO	P50528 schizosacch
15	247	5.2	502	1	RK11_SECFE	Q02723 secale cere
16	246	5.2	548	1	AAK1_RAT	P54645 rattus norv
17	245	5.2	646	1	CKK_MOUSE	Q94454 homo sapien
18	245	5.2	556	1	SPAK_HUMAN	Q92149 mus musculu
19	239	5.1	443	1	MRK_ARATH	P43294 arabidopsis
20	238.5	5.1	372	1	SPK1_SCHPO	P27636 schizosacch
21	237	5.0	371	1	MMK2_MEDSA	Q43533 medicago sa
22	235.5	5.0	713	1	KP78_HUMAN	P24248 homo sapien
23	235	5.0	372	1	NTEF3_TOBAC	Q40517 nicotiana t
24	231.5	4.9	1062	1	CC7_SCHPO	P41892 schizosacch
25	231	4.9	774	1	KPKK_MOUSE	Q00512 mus musculu
26	231	4.9	1130	1	ABL1_HUMAN	P00519 homo sapien
27	229.5	4.9	603	1	PKR1_HUMAN	P53350 homo sapien
28	228.5	4.8	1518	1	KRK1_YEAST	P34244 saccharomyc
29	228	4.8	1382	1	INSR_MOUSE	P06213 homo sapien
30	227.5	4.8	779	1	SNL_MOUSE	Q06070 mus musculu
31	227	4.8	376	1	MPK4_ARATH	Q39024 arabidopsis
32	227	4.8	552	1	AAK2_HUMAN	P54646 homo sapien
33	227	4.8	552	1	AAK2_RAT	Q09137 rattus norv

34	226.5	4.8	303	1	CDK4_HUMAN	P11802 homo sapien
35	226.5	4.8	915	1	KCC4_YEAST	P25389 saccharomyc
36	226	4.8	395	1	MPK6_ARATH	Q39026 arabidopsis
37	225.5	4.8	292	1	CC2H_DICDI	P34117 dictyostell
38	225	4.8	296	1	CDG2_DICDI	P34112 dictyostell
39	224.5	4.8	603	1	PLK1_MOUSE	Q07832 mus musculu
40	224	4.7	376	1	MPK2_ARATH	Q39022 arabidopsis
41	223.5	4.7	384	1	MAPK_PETHY	Q40884 petunia hyb
42	223.5	4.7	974	1	CC1_YEAST	P27636 saccharomyc
43	222.5	4.7	714	1	HUNK_HUMAN	P57058 homo sapien
44	222.5	4.7	746	1	ABL_MIVAB	P00521 abelson mur
45	222.5	4.7	776	1	SNL1_RAT	Q9105 rattus norv

ALIGNMENTS

RESULT 1	SNF1_CANCA	STANDARD:	PRT:	611 AA.
AC	Q00372:			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	Carbon catabolite derepressing protein kinase (EC 2.7.1.1).			
GN	SNF1.			
OS	Candida glabrata (Yeast) (Torulopsis glabrata).			
OC	Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetaceae;			
OC	Saccharomycetales; mitosporic Saccharomycetales; Candida.			
NC	NCBI_TaxID=5478;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRATIN-NCCLS84;			
KX	MEDLINE=97101049; Pubmed=8945576;			
RA	Petier R., Kwon-Chung K.J.;			
RT	"Disruption of the SNF1 gene abolishes trehalose utilization in the			
RT	pathogenic yeast Candida glabrata.";			
RL	Infect. Immun. 64:5269-5273(1996).			
CC	-1- FUNCTION: ESSENTIAL FOR RELEASE FROM GLUCOSE REPRESSION. IT			
CC	INTERACTS AND HAS FUNCTIONAL RELATIONSHIP TO THE REGULATORY			
CC	PROTEIN SNF4. COULD PHOSPHORYLATES CAH8 (BY SIMILARITY).			
CC	-1- SUBCELLULAR LOCATION: ASSOCIATED WITH THE NUCLEAR MEMBRANE (BY			
CC	SIMILARITY).			
CC	-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.			
CC	SNF1 SUBFAMILY.			
CC	-----			
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CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL: L78130; AAB48642.1; -			
DR	HSSP: P00518; 2PHK.			
DR	InterPro: IPR000719; Euk_PKinase.			
DR	InterPro: IPR002290; Ser_thr_kinase.			
DR	Pfam: PF00069; pkinase.1.			
DR	SMART: SM00220; S_TKC.1.			
DR	PROSITE: PS00107; PROTEIN_KINASE_ATP.1.			
DR	PROSITE: PS00108; PROTEIN_KINASE_ST.1.			
DR	PROSITE: PS50011; PROTEIN_KINASE_DPM.1.			
KW	Transferase; Serine/threonine-protein kinase; ATP-binding;			
KW	Phosphorylation; Carbohydrate metabolism; Nuclear protein.			
FT	DOMAIN 6 17			
FT	DOMAIN 39 290			
FT	NP_BIND 45 53			
FT	BLINDING 68 68			
FT	ACT_SITE 161 161			
FT	MOD_RES 194 194			
SD	SEQUENCE 611 AA; 70049 MW; 89E17812A4900CD0 CRC64;			

Query Match 6.1% Score 286.5; Pos 1; Length 611;
 Best Local Similarity 20.8%; Prod. No. 7.9e-12;
 Matches 111; Conservative 120; Mismatches 231; Indels 165; Gaps 25;

07 9 MGAPFASALPHVYVNSGLPTNSTRKTLGRQLTKTTHPRQLQVVD 58
 10 45 LKESSEKVKIAYVTVCKVKAKSKNKVKLAKSDGGRDDELSYRLDHPHILKLD 104
 07 59 LKESKHKIYVAVDEFESELEDEKRVSGSTVLAIPVLOGLQVNNKIGLVHVALS 118
 10 105 VIKSKDE LHWLEFVANNLELTVYGRKKSGSGGRARRPVQGLTSNVEGCHHKLVHRLK 163
 07 119 PGNILLKRGKIKLAKPELVYKTAHGVDPVIGTSLAPLVAGGLFKTTDMSSKRP 178
 10 164 PGNILLKRGKIKLAKPELVYKTAHGVDPVIGTSLAPLVAGGLFKTTDMSSKRP 212
 07 179 LPSHKSIVWGLGILFEELVGRKLYGSLDSEKPELTTLVYQGLVLAEEFEKGL 236
 10 213 AGPEVYVWSSGVTLVYVLGRKLP.....DEESLPVLPKNSGVV 253
 07 247 DITKLPETVITLANKCLFPHSKAPPTDDEMKKVESESVATPTKVASLSSSLGR 296
 10 294 TLKPLSPVASDLKRMILVNPINLSLHMODERFKVID 294
 07 297 ADLTPPELSQIKOLNNIYLAERSLEVVYLAELAGDEKELVKNELTKSKPTCTLP 356
 10 299 AAVLYVQILKQGFQFNKSKNSGVNVEELDEEV.....VLISK 333
 07 337 NTLPEKSSPVGGGRSSSL LADTVTLSSVGRNKLKIVGQAVPLLEHQSINLP 413
 10 334 MGCDKDEYVALSSSEDPVAVNELRNAYLIRKNSLIRK 373
 07 414 SNSNNELSAVALDPLLEKDEYVGNKLEDEKLKAVYKNQLKREAV 465
 10 424 MGQNNVT GELDFELSGSPTEPQNG EKAKSEHQQKSKSKSLASVQGRVF 427
 07 466 DITKLPKRLVWALGVVAVIHAQVADIKDTPTTQGLVNDITKQYQDELSPPH 525
 10 428 PGLPGRPDQSKKE DSTSTPESLQVIRKMLADGLPAA 465
 07 526 AKPEVILKAWVSHDELYWV GLESLVAPFLYLNINNNALVAVMSAFL 574
 10 466 SKI SPVYKSKTGMHFGTKRSVPLVGMCHVIALKILGAVMANSEELWTR 520
 07 575 PKYVNFYKNSNIVQYEL TVFSQMLAFHPELSNHLNGVF 617
 10 521 VWKATD SPSKSLDEYVKKTFMLKFLVQLFQLENNVLDGRF 564

RESULT 2
 SNF1 CANTR
 10 SNF1 CANTR STANVADQ; POS: 619 AA.
 10 094168;
 10 15 JUL 1999 (601, 49, (created)
 10 15 JUL 1999 (601, 48, (last sequence update)
 10 15 JUL 1999 (601, 48, (last annotation update)
 10 106 can be evaluated to degrading protein kinase (eg 2.7.1.-);
 08 SNF1
 08 Candida tropicalis (Yeast);
 08 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 08 Saccharomycotales; mitospore Saccharomycotales; Candida.
 08 NCBI TaxID 5482;
 08 11;
 08 SUGGESTED FROM N.A.
 08 Kawai T., Oshima K., Oeda M., Tanaka A.;
 08 "Genetic evaluation of the function of SNF1 in Candida tropicalis";
 08 submitted (Mar 1999) to the EMBL/Genbank/DBJ databases;
 08 FUNCTION: ESSENTIAL FOR RELEASE FROM GLUCOSE REPRESSION. IF
 08 INTERACTS AND HAS FUNCTIONAL RELATIONSHIP TO THE REGULATORY
 08 PROTEIN SNF4, COULD PHOSPHORYLATES CATH (BY SIMILARITY).
 08 SUBCELLULAR LOCATION: ASSOCIATED WITH THE NUCLEAR MEMBRANE (BY
 08 SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC SNF1 SUPERFAMILY.

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 CC or send an email to license@sib.scrib.ch).

DR PML: AH024535; BA075889.1; -;
 DR HSPD: P03132; IAPM.
 DR InterPro: IPR000713; Ser_Pkinase.
 DR InterPro: IPR002290; Ser_Thr_Pkinase.
 DR Pfam: PF00069; Pkinase_1.
 DR SMART: SM00220; S_TKc_1.
 DR PROSITE: PS00107; PROTEIN KINASE ATP_1.
 DR PROSITE: PS00108; PROTEIN KINASE ST_1.
 DR PROSITE: PS50011; PROTEIN KINASE_DOM_1.
 KW Transferrase; Serine/threonine-protein kinase; ATP-binding;
 KW phosphorylation; Carbohydrate metabolism; Nuclear protein.
 FT DOMAIN 17 29 POLY-HIS.
 FT DOMAIN 52 403 PROTEIN KINASE.
 FT BINDING 58 66 ATP (BY SIMILARITY).
 FT BINDING 81 81 ATP (BY SIMILARITY).
 FT ACT SITE 174 174 BY SIMILARITY.
 FT MOD RES 207 207 PHOSPHORYLATION (AUTO) (BY SIMILARITY).
 SQ MOD RES 207 207 OCCTFCDEGTDDZDGRGCA;
 SNORANCE 619 AA; 70323 MW; 0PC1FCDEGTDDZDGRGCA;

Query Match 6.0% Score 282; Pos 1; Length 619;
 Best Local Similarity 21.8%; Prod. No. 1.6e-11;
 Matches 111; Conservative 74; Mismatches 150; Indels 176; Gaps 15;

07 29 LPTP--NSIKILKRPDEKT 47
 10 47 LPTPNNVNNRIRVYQILKTLGSGSKYKYLADHVGSGQVAKLITNKETLAKSDGGR 96
 07 48TTPRLQVYVDSKGRKRLVYVAVDEFESELEDEKRVSGSTVLA 97
 10 97 VERELSYRLKLBHPLIKIYVAKSDQ LTMVLEFAGKELFVYVGRKMPDEARFP 155
 07 98 FEVLQGYQMKHCHVRAISPNHILDRKQIKLAKELGYHMTAGVNDVDFPGYSYL 157
 10 156 QVILAAVEYVGRKLVHRLKPEMLLLDQKLVNKLAFGLSNIMTGNFTKSGSINVA 215
 07 158 APEVLAQGIKTTIMPSKRLDNGKSDVSGATILEFLVGRKLPQSLDLSERKEL 217
 10 216 APEVLSKLYAGPEVDWSSGVTLVYVMDGRPDDEFTATERRK 261
 07 218 TLDPVDELVLAEHAGTDLIKELPEVITLANKCLFPHSKAPPTDDEMKKVESEV 277
 10 262SNVYTPVNTLSFGAKHLLTRMLVANNLNTTHHEIMEDHWRKQIM 307
 07 278 PLTPTRKPSLSSSSIKCAMLTLEPDISOLCKDINNDYLAERSTEYVYL 328
 10 308 P.....DYLLPELSIKTSKTLIDELVLSALSVTMDGYRDELISV 348
 07 329WELAGDLK---ELVNNKELIRSKRP 351
 10 349 LKANKRAAAGATAPVWQSKSNVLAVALYLMKNHNTVLDKSSKSENESELSLSP 408
 07 452 LCTLPNELPEGSEFPQGRGRSSSLADPTVYVSLVGRNKLKIVGQAVPLLEHQSIN 411
 10 409 SSSSEFNPGSTSSACVQGSTVYGLAVPQSTSL 442
 07 412 PHSNNNELSAVALDPLLEKDEYVGN 440
 10 443 PNLTALPLSLSLHRAVMMETKVN 468

RESULT 3

G1N4_YEAST STANDARD: PRT: 1142 AA.

AC G12263:

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Serine/threonine-protein kinase G1N4 (EC 2.7.1.-).

GN G1N4 OR YD8507C OR D9719.13.

OS Saccharomyces cerevisiae (Baker's yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomycetes.

OX NCBI_TaxID=4932:

RN (1)

RP SEQUENCE FROM N.A.

RX MEDLINE=94030835; PubMed=9814093:

RA Longtine M.S., Fares H., Pringle J.R.:

RT Role of the yeast G1N4 protein kinase in septin assembly and the

KT relationship between septin assembly and septin function.*:

RL J. Cell Biol. 143:719-736(1998).

RN (2)

RP SEQUENCE FROM N.A.

RA Dietrich F.S., Mulligan J., Allen E., Araujo R., Aviles F., Berno A., Carpenter J., Chen E., Cherry J.M., Chung E., Duncan M., Hunkeler-Smith S., Hyman R., Komp C., Lashkari D., Lew H., Lin D., Mosedale D., Nakahara K., Namath A., Oelner P., Oh C., Petel F.X., Roberts D., Schramm S., Schroeder M., Shogren T., Shroff N., Wiant A., Yelton M., Botstein D., Davis R.W.:

RA Submitted (Aug-1995) to the EMBL/Genbank/DBJ databases.

CC - FUNCTION: MAY PLAY A ROLE IN SEPTIN ASSEMBLY.

CC - SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC NIM SUBFAMILY.

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CC

DR EMBL: U33140; AAA75513.1:

DR EMBL: U33057; AAB64949.1:

DR HSSP: P36897; 1TH1.

DR SGD: S0002915; G1N4.

DR InterPro: IPR000719; Euk_Pkinase.

DR InterPro: IPR002290; Ser_thr_Pkinase.

DR Pfam: PF00069; Pkinase; 1.

DR SMART: SM00220; S_TKc; 1.

DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.

DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.

DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.

KW Transferase; Serine/threonine-protein kinase; ATP-binding.

FT DOMAIN 19 289 PROTEIN KINASE.

FT NP_BIND 25 33 ATP (BY SIMILARITY).

FT BINDING 48 48 ATP (BY SIMILARITY).

FT ACT_SITE 156 156 BY SIMILARITY.

FT ACT_SITE 156 156 BY SIMILARITY.

SO SEQUENCE 1142 AA; 129857 MW; E016FF4B84DD811 CRC64:

Query Match 5.9%; Score 280; DB 1; Length 1142;

Best Local Similarity 24.9%; Pred. No. 5, 2e-11;

Matches 104; Conservative 70; Mismatches 147; Indels 96; Gaps 16;

DB 84 IMKLINPVLRLYDWEINTD-LYLVLEAKGELPNNLVEGRPLPEHAIREFPOTIT 142

QY 103 GI4YMKKGLIVRALSHNLLDKKGIKAKGLYHMTANGDPPIGYSPYLAPEVI 162

DB 143 GVSAYGALGIVHNDIKPENLLDKKNIKIAIDGMALEHESGLLETSGSPYAPAEIV 202

QY 163 AGQIFKTDHPSKKPLP-SGPKSDVWSIGILLPELCVGSKLEQSLDISERKELLTLDG 221

DB 203 S-----GIPYGFASDVWSCGVLFPALLTGLRPFDEPDGNIR----- 239

QY 222 VDDTLIVAEHGGCLDIK--ELPETVIDLANKCTFHPSKRPDPDELMKDKPSEVS-- 277

DB 240 ----TLKKVKGEEFEMSDPISREAODLIRKILITVDPERIRKTRDILKPHILQKIPSI 295

QY 278 -----PIYTFPTKASTFSSSLRCADTL-----PDISQLCKDINDY 316

DB 296 RDSKIRGLPREDIYLLTSLSSNSI---IATIIQN.VILMHGDPPIKIKLHPGAN- 351

QY 317 LAENSIEFVYVLM-QIAGDILKELVNEKILRSKPP-----CLPNIPLPDEG 364

DB 352 -AEKTLVALLYRFGK---DIQKELIKOOQVKRQSISSVSPSKRVSTPQ----- 399

QY 365 SFGGGRDSSLLDITVTLSCGLRNRIKDYGGAFVYLLDDGSLNPHSNNEL 421

DB 400 ---RRNHESLISVTS-----SRKKPIPFKKF-TASSASSNLITPSSRRLS 443

RESULT 4

SNFL_SCHPO STANDARD: PRT: 576 AA.

AC 074536:

DT 15-JUL-1999 (Rel. 38, Created)

DT 15-JUL-1999 (Rel. 38, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE SNFL-like protein kinase (EC 2.7.1.-).

GN SPCG74.03C.

OS Schizosaccharomyces pombe (fission yeast).

OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae;

OC Schizosaccharomycetes.

OX NCBI_TaxID=4896:

RN (1)

RP SEQUENCE FROM N.A.

RC STRAIN=972;

RA Murphy L., Harris D., Lyne M., Rajandream M.A., Barrell B.G.:

RL Submitted (SEP-1998) to the EMBL/Genbank/DBJ databases.

CC - SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC SNL SUBFAMILY.

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CC

DR EMBL: AL031543; CAA20833.1:

DR HSSP: P00518; 1PHK.

DR InterPro: IPR000719; Euk_Pkinase.

DR InterPro: IPR002290; Ser_thr_Pkinase.

DR InterPro: IPR000449; DBA.

DR Pfam: PF00069; Pkinase; 1.

DR SMART: SM00220; S_TKc; 1.

DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.

DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.

DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.

KW Transferase; Serine/threonine-protein kinase; ATP-binding.

FT DOMAIN 34 285 PROTEIN KINASE.

FT NP_BIND 40 48 ATP (BY SIMILARITY).

FT BINDING 63 63 ATP (BY SIMILARITY).

FT ACT_SITE 156 156 BY SIMILARITY.

FT ACT_SITE 156 156 BY SIMILARITY.

SO SEQUENCE 576 AA; 65996 MW; F5857B8P171E7B50 CRC64:

Query Match 5.8%; Score 275; DB 1; Length 576;

Best Local Similarity 21.3%; Pred. No. 4, 3e-11;

Matches 122; Conservative 96; Mismatches 202; Indels 154; Gaps 21;

QY 45 LKTIHPRICGVVDISRGKHERLVVAHGERSLIEDLLRKKPVSGSVLCIAFEVLDL 104


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RESULT 6
SNF1_YEAST
ID SNF1_YEAST STANDARD: PRT: 633 AA.
AC p06782;
DT 01-JAN-1988 (Rel. 06, last sequence update)
DT 01-JAN-1988 (Rel. 06, last sequence update)
DT 15-JUL-1999 (Rel. 48, last annotation update)
DE Carbon catalytic derepressing protein kinase (EC 2.7.1.-).
OS SNF1 OR CACT1 OR CCR1 OR PAS14 OR GIC2 OR YDR477W OR DB035.20.
CN Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
XX MBI_TaxID=4932;
XX
XX SEQUENCE FROM N.A.
XX MEDLINE=86289453; PubMed=3526554;
XX Celera J.L., Carlson M.;
XX "A yeast gene that is essential for release from glucose repression
XX encodes a protein kinase.";
XX Science 233:1175-1180(1986).
XX
XX [2]
XX SEQUENCE FROM N.A.
XX Dietrich F.S., Mulligan J., Allen E., Araujo R., Ayiles E.,
XX Betno A., Carpenter J., Chen E., Cherry J.M., Chung E., Duncan M.,
XX Hunicke-Smith S., Hyman R., Kemp C., Laskikari D., Law H., Lin D.,
XX Mosedale D., Nakahara K., Namath A., Oefner P., Oh C., Patel F.X.,
XX Roberts D., Schramm S., Schroeder M., Shogren T., Stroff N.,
XX Whitant A., Yellon M., Borstein D., Davis R.W.;
XX Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
XX
XX [3]
XX SEQUENCE OF 274-284; 528-539 AND 622-630, AND PHOSPHORYLATION SITE.
XX MEDLINE=9411988; PubMed=7905477;
XX Mitchellhill K.L., Stapleton D., Gao G., House C., Mitchell H.,
XX Katsis F., Witters L.A., Kemp R.E.;
XX "Mammalian AMP-activated protein kinase shares structural and
XX functional homology with the catalytic domain of yeast Snf1 protein
XX kinase.";
XX J. Biol. Chem. 269:2361-2364(1994).
XX
XX [4] FUNCTION: ESSENTIAL FOR RELEASE FROM GLUCOSE REPRESSION. IT
XX INTERACTS WITH AND HAS FUNCTIONAL RELATIONSHIP TO THE REGULATORY
XX PROTEIN SNF4. INTERACTS ALSO WITH S1P1, S1P2 AND GAL83. COULD
XX PHOSPHORYLATES CATA.
XX
XX [5] SUBCELLULAR LOCATION: ASSOCIATED WITH THE NUCLEAR MEMBRANE.
XX
XX [6] SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
XX SNF1 SUBFAMILY.
XX
XX -----
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XX
XX -----
XX EMBL: M13971; AAA35058.1;
XX EMBL: U33050; AAB64904.1;
XX PIR: A26030; A26030.
XX HSSP: G63450; IAO6.
XX SGD: S0002885; SNF1.
XX InterPro: IPR000719; Euk_Pkinase.
XX InterPro: IPR002290; Ser_Thr_Pkinase.
XX Pfam: PF00069; Pkinase.1.
XX SMART: SM00220; S_TKc; 1.
XX PROSITE: PS00107; PROTEIN_KINASE_ATP_1.
XX PROSITE: PS00108; PROTEIN_KINASE_ST_1.
XX PROSITE: PS00111; PROTEIN_KINASE_DOM_1.
XX Transferrase; Serine/threonine-protein kinase; ATP-binding;
XX Phosphorylation; Carbohydrate metabolism; Nuclear protein.
XX
XX DOMAIN 18 32 POLY-HIS.
XX NP_BIND 55 306 PROTEIN KINASE.
XX BINDING 61 69 ATP (BY SIMILARITY).
XX BINDING 84 84 ATP (BY SIMILARITY).
XX ACT_SITE 177 177 HY SIMILARITY.

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FT MOD_RES 210 210 PHOSPHORYLATION (AUTO-);
SQ SEQUENCE 633 AA; 72045 MW; F5C63565C986CAE3 CRC64;
Query Match 5.7%; Score 268; DB 1; Length 633;
Best local Similarity 24.1%; Pred. No. 1.5e-10;
Matches 92; Conservative 71; Mismatches 130; Indels 88; Gaps 13;
45 LKTIHPRLCQYVYDISRQKHERLVVAEHCERSELEDLRHKPKVSGSTVLCIAFEVIAQGL 104
DB 107 LRLRHHRHLIKLYDVIRSKDF-IIMVIFVAGNGLFPIYVQROKMSQGEARRFQQLISAV 165
OY 105 QYNNKMGIVHRAISPHNILLDRKGHLKLAGSLYHMTARQDDVDPPIGYPSVLAPEVIAQ 164
DB 166 EYCHRRKIVAROLDKPEHLIDDEHLMVADFGSLNMTDGNFLKTSQSGSPNVAAPFVIG 225
OY 165 GFRKTDHMRSKKPLPSGPKSDVWSIGIILFELCVGRKLI.FQSLDISDEBLKLTLLTCVDD 224
DB 226 KLY-----AGPEVDVWSCGVILYV-----LCRRLPF-----DDE 255
OY 225 TLIVLAE--EHGCLDLIKELPETVIDLANKCLTFHPSKRPDPDLKKDVFSEVSPLY-- 280
DB 256 SIYLFENINISNGVYTLPRFLSPGAGLIKRLVLNPLNRISHHIMQDPMFKVDLEYL 315
OY 281 TPTTPASLFSSSILKCADLILPEDISQKIDINDYLAERSIEVYVYLMKLAGGLEKEL 340
DB 316 PDLKLPH-----PEPENE-----NNDSSKKDGSPPD-----NDEIDNLI 348
OY 341 VNKETIFSKRPICITLPNLFPEDESFGQGRSSILDDITVTLISQLRHMLKDVGGHAF 400
DB 349 VN--ILSS-----TMGYEKDFIVESLESSEDTDAF-----NEIRDA----- 382
OY 401 YPLLEDDQSNIPHSNNSNELS 421
DB 383 YMLIKENKSLIKDKMKANKSVS 403
RESULT 7
CDK6_HUMAN
ID CDK6_HUMAN STANDARD: PRT: 326 AA.
AC G000534;
DT 01-APR-1993 (Rel. 25, last sequence update)
DT 01-APR-1993 (Rel. 25, last sequence update)
DT 16-OCT-2001 (Rel. 40, last annotation update)
DE Cell division protein kinase 6 (EC 2.7.1.-) (Serine/threonine-protein
DE kinase p151B).
CN CDK6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
XX NCBI_TaxID=9606;
XX
XX [1]
XX SEQUENCE FROM N.A.
XX MEDLINE=92347325; PubMed=1639063;
XX Mayerson M., Enders G.H., Wu C.-L., Su L.-K., Gorka C., Nelson C.,
XX Harlow E., Tsai L.-H.;
XX "A family of human cdc2-related protein kinases.";
XX EMBO J. 11:2909-2917(1992).
XX
XX [2]
XX SEQUENCE OF 180-326 FROM N.A.
XX
XX RA Pauley A.;
XX Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
XX
XX [3]
XX X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF COMPLEXES WITH INK4A AND
XX INK4D.
XX MEDLINE=98421670; PubMed=9751050;
XX Russo A.A., Tong L., Lee J.O., Jeffrey P.D., Pavletich N.P.;
XX "Structural basis for inhibition of the cyclin-dependent kinase Cdk6
XX by the tumour suppressor p16INK4a.";
XX Nature 385:237-243(1998).
XX
XX RL Nature 385:237-243(1998).
XX
XX CC -1- FUNCTION: PROBABLY INVOLVED IN THE CONTROL OF THE CELL CYCLE.
XX INTERACTS WITH D-TYPE G1 CYCLINS.
XX
XX CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

```


QY 84 SCSTVIAIAFEVLOGLQYMKHGIHRAKALSPENILDLDRKGIKAKFGUYHTMTAGDDVD 148
 DB 167 EEAIIATILKEVLEGLDYLHNRGQIHRDLKANILILGHGQVADPEVSALATGGVYT 226
 QY 149 FP-----IGVSYIAPEVIAOGIFKTTDHMSKRLPSGPKSDVWSIGITILFELCYGRK 202
 DB 227 RNRKREIVGTPGMAPEVMEQ-----VRGYDF-----KADMSFGITAIELATGAA 273
 QY 203 LFQSDISERIKELITDQVDDTLVLAEHGGIDITIKELPEVITDLINKLCTIFPSPRRP 262
 DB 274 PHKTPPMKVL--KTLNDPPLLETGVEDK--EMMKKYGSFPRKLLSLCTQKDPKRRP 328
 QY 263 IPDELKRVSESEVSPLYTPFKPASTLFSSSLKCADLILPEISQICDI-----NNYVL 317
 DB 329 TAAELKCKCFQK-----AKNREYLIELK-----LITPTDIAKRAKVRKVRKPSGHL 376
 QY 318 AERSIEEYVYIMGLAGGLEKELVKKELIRSKPPICTLPNLEEDGE--SPGQGRDSSIL 376
 DB 377 --HKTHGIDMEWS-----DDEMDKES-----EFGKAAFSQEKSRBAYE 412
 QY 377 IDDTVTLSLQGLRNLKQVGGAEAFYPLEDDQSNLPHSNNELSAATLPLITREKOTE 436
 DB 413 ENPEIAVASASTIPEQIQS-----LSVHDSQGPNNAEVREASSCAVINLRLNSR 464
 QY 437 YQINRI-----LTF-----DRLKAYPKKQIMKEARVDIPPIMR 472
 DB 465 KELNDIRREFTPGKRTADGVSELFSAGLVDSGHVIVANAIQK-----IVDDPKALK 517
 QY 473 GLTMAALLGVEGA 485
 DB 518 TLTFKIASGCDGS 530

RESULT 9

CNK_RAT
 ID CNK_RAT STANDARD: PRT: 615 AA.
 AC Q9R011:
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Cytokine-inducible serine/threonine-protein kinase (EC 2.7.1.37) (FGF-
 DE Inducible kinase) (Fragment).
 CN CNK OR FPK.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxId=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-99452760; PubMed-10523297;
 RA Kauselmann G., Weiler M., Wulft P., Jessberger S., Konietzko U.,
 RA Scaldi J., Staudl U., Beretler-Hahn J., Strehardt K., Kuhl D.;
 RT "The polo-like protein kinases Pnk and Snk associate with a Ca(2+)-and
 RT integrin-binding protein and are regulated dynamically with synaptic
 RT plasticity.";
 RL EMBO J. 18:5528-5539(1999).
 CC -1- FUNCTION: SERINE/THREONINE PROTEIN KINASE INVOLVED IN REGULATING M
 CC PHASE FUNCTIONS DURING THE CELL CYCLE. MAY ALSO BE PART OF THE
 CC SIGNALING NETWORK CONTROLLING CELLULAR ADHESION. IN VITRO, IS ABLE
 CC TO PHOSPHORYLATE CDC25C AND CASEIN (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein -> ADP + a phosphoprotein.
 CC -1- SUBUNIT: BINDS TO THE CALCIUM/INTEGRIN-BINDING PROTEIN (Cib). THIS
 CC INTERACTION PROBABLY OCCURS VIA THE POLO-BOX DOMAIN.
 CC -1- SUBCELLULAR LOCATION: WHEN INDUCED, IT TRANSLOCATES INTO THE
 CC DENDRITES OF ACTIVATED NEURONS.
 CC -1- TISSUE SPECIFICITY: CONSTITUTIVELY EXPRESSED IN POST-MITOTIC
 CC NEURONS.
 CC -1- INDUCTION: BY THE INTENSE ACTIVITY ASSOCIATED WITH SEIZURES.
 CC -1- PTM: PHOSPHORYLATED AS CELLS ENTER MITOSIS AND DEPHOSPHORYLATED AS
 CC CELLS EXIT MITOSIS (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC CDC5/POLO SUPERFAMILY.

CC -1- SIMILARITY: CONTAINS 2 POLO BOX DOMAINS.
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 DB EMBL: AF136584; AAF08467.1;
 DR InterPro: IPR000719; Euk_Pkinase.
 DR InterPro: IPR000959; POLO_box.
 DR InterPro: IPR002291; Phosph_kin_gamma.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR InterPro: IPR001245; Tyr_kinase.
 DR Pfam: Pf00069; Pkinase.1.
 DR Pfam: Pf00659; POLO_box.2.
 DR PRINTS: PRO1049; PHOSPHKINASE.
 DR PRINTS: PRO0109; TYRKINASE.
 DR SMART: SMO0220; S_TKc.1.
 DR PROSITE: PS50078; POLO_BOX.2.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP.1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM.1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST.1.
 DR Transferrase: Serine/threonine-protein kinase: ATP-binding; kepeat;
 KW Phosphorylation.
 FT NON_TER 1 1
 FT DOMAIN 31 283 PROTEIN KINASE.
 FT NP_BIND 37 45 ATP (BY SIMILARITY).
 FT BINDING 60 60 ATP (BY SIMILARITY).
 FT ACT_SITE 154 154 BY SIMILARITY.
 FT DOMAIN 440 503 POLO BOX 1.
 FT DOMAIN 537 607 POLO BOX 2.
 FT NON_TER 615 615
 SQ SEQUENCE 615 AA; 68800 MW; 06584C22985D71BD CRC64;

Query Match 5.4k; Score 257; DR 1; Length 615;
 Best Local Similarity 21.28; Pred. No. 7.7e-10;
 Matches 141; Conservative 94; Mismatches 241; Indels 188; Gaps 26;

QY 35 SIKILGRPOLIKTIHHPILCOYDHSRC-KHPRIVVAERHCE-----RSLE 79
 DB 58 AVKVPQSRVAKPHQREKILNEIEIHRLOJRHRYVRSHHEEDADNIYIELECSKSLA 117
 QY 80 DLLREKRPVSCSTVIAFEVLOGLQYMKHGIHRAKALSPENILDLDRKGIKAKFGUYHTMTAGDDVD 148
 DB 118 HIKRKARHTLLEPEVARYYLKQIISGLKYLHQRGILHRDLKLGPNFJTNMELKAGCPGIAA 172
 QY 140 MTAHDDVDVFL-GYPSYLADEV-IAOGIFKTTDHMSKRLPSGPKSDVWSIGITILFEL 197
 DB 178 RLEPPEQKKTKTCGPNVAPEVLLRQ-----HGPEADVWSIGCWYTL 222
 QY 198 CVGRKLFQSDISERIKELITDQVDDTLVLAEHGGIDITIKELPEVITDLINKLCTIFPSPRRP 262
 DB 223 LCGSPPEFADLKE-----TYRCL-----KQVHTLPASLSIPAR-QLLAAILRAS 267
 QY 258 PSKRPTPELMKDKVSESVSPLYTPFKPASTLFSSSLKCADLILPEISQICDI-----NNYVL 317
 DB 268 PDRPSIQILRHDFETK-----YTPDRLPV-----SSCVTPDLPFPNARSILFAKVTSLF 321
 QY 318 AERS-----IEEYVYIMGLAGGLEKELVKKELIRSKPPICTLPNLEEDGE--SPGQGRDSSIL 376
 DB 322 GRRKSKNNHSEEDQNVGLVSGLMRTSIGHPDVAPPAASALAPSVLTAEDSSPR 381
 QY 362 -----DGSEFGQGRSSILDDITVTLSLQGLRNLKQVGGAEAFYPLEDDQSNLPHSNNELSAATLPLITREKOTE 436
 DB 382 GLASSGQGFEG-----LTVTVESALCALRMV-----AMPAPAEQAPAL----- 425
 QY 417 NNELSAATLPLITREKOTE-----YQINR-----LTF-----DRLKAYPKKQIMKEARVDIPPIMR 472
 DB 426 -----AOPELWVSKWVDVSNKPGFGYOLSSRRVAVLPMGTHMALSAKKKTVHYNPT 479


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QY 200 GKLEFQSLDISEKLELLTLKVDOTLIVLAHEGCLDIKELPTVIDLLNKLCTFHPS 259
DB 213 GLTPEDDENIPVLFKKI-----KCGITLTPSLSGANDLIPRMVLVDPM 257
QY 260 KRPTDELKQKQVSEVSPITPTFKPASLFSSSLRCADLTLPEDISOLCNDINDYAE 319
DB 258 KRVTLPELRQHPFQAHLPRLVAVP-----PPTVQQAKKIDFELL-- 298
QY 320 KSTEVYTLKWLACGLDERKLVNKKELIRSKPPICLTPNPLFEDGESFGQGRDSSLDDT 379
DB 299 -----QEVIN-----MGFDRLNHLIE-- 313
QY 380 TVTSLCOLRNKLDVGEAEFPLEDD 406
DB 314 -----SLRNFTQNDGTIVYLLIDN 333

RESULT 11
CC5_YEAST STANDARD: PRT: 705 AA.
ID CC5_YEAST
AC P32562;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cell cycle protein kinase CDC5/MSD2 (EC 2.7.1.-).
GN CDC5 OR PKX2 OR MSD2 OR YMR001C OR YMR0270.03C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=A364A;
RX MEDLINE=93309479; PubMed=8321244;
RA Kitada K., Sugino A., Johnston L.H., Johnson A.L.;
RA *A multicopy suppressor gene of the Saccharomyces cerevisiae G1 cell
RI cycle mutant gene dbf4 encodes a protein kinase and is identified as
RT CDC5.*
RL Mol. Cell. Biol. 13:4445-4457(1993).
RN 12
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RA Devlin K., Churcher C.M., Bartell B.G., Rajandream M.A., Walsh S.V.;
RA Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
CC 1- FUNCTION: PROTEIN KINASE REQUIRED FOR THE CELL CYCLE.
CC 1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC 1- CDC5/POLQ SUBFAMILY.
CC 1- SIMILARITY: CONTAINS 2 POLQ HOX DOMAINS.
CC -----
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CC -----
DB EMBL: M84220; AAA02576.1;
DB EMBL: Z48613; CAA8516.1;
DB PIR: S27445; S27445.
DB HSSP: P05132; IATP.
DB SGP: S0004603; CDC5.
DB InterPro: IPR000719; Euk_Pkinase.
DB InterPro: IPR000959; POLQ_Box.
DB InterPro: IPR002290; Ser_thr_Pkinase.
DB Pfam: PF00659; Pkinase.1.
DB Pfam: PF00659; POLQ_Box.2.
DB SMART: SM00220; S_TKc.1.
DB PROSITE: PS50078; POLQ_HOX.2.
DB PROSITE: PS00107; PROTEIN_KINASE_ATP.1.
DB PROSITE: PS50011; PROTEIN_KINASE_DOM.1.
DB PROSITE: PS00108; PROTEIN_KINASE_ST.1.

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KW Cell cycle; Cell division; Serine/threonine-protein kinase;
KW Transferase; ATP-binding; Repeat.
FT DOMAIN 82 337 PROTEIN KINASE.
FT NP_BIND 88 96 ATP (HY SIMILARITY).
FT BINDING 110 110 ATP (HY SIMILARITY).
FT ACT_SITE 204 204 BY SIMILARITY.
FT DOMAIN 520 587 POLQ BOX 1.
FT DOMAIN 619 692 POLQ BOX 2.
SO SEQUENCE 705 AA; 81030 MW; B5A25F1B8BAAAD3C CIRC04;

Query Match 5.38; Score 252; DB 1; Length 705;
Best local similarity 22.38; Pred. No. 26-09;
Matches 144; Conservative 108; Mismatches 241; Indels 154; Gaps 28;

QY 37 KILGFQILKTIIPRLCOYVDISGRGHERLVVAEGER-SLEDLREKPPVSCSTVLC 95
DB 125 KILSEIQHKSMSPHNIIVQFDCE-IDSNNYILLEICPNSSIMELIKRRKVLTEPEVRF 183
QY 96 IAFVILQGLQYMNKKGIVHRAISPHNILLPRKKGHLKAKVGLYMTAGDVDFPI-GYP 154
DB 184 FTTQTCGAIKYMHSRVIHRLKLGNIFFDSNYNLKIGDFGLAAVLANESERKTYICGTP 243
QY 155 SYLAPVIAQGIPTTTHMPKRPISGPKSDVWSIGIILPELVGKGLFQSLDIS--E 211
DB 244 NYIAPEVL--MGKHSCH-----SPYVDIMSLGMLYKALLIGKPPQARDVNTIYE 291
QY 212 KLKFLTLDCVDDIIVLAHEGCLDIKELPTVID--LANKLIFHPSKRPDPDEL 267
DB 292 RIK-----CRDSFPRDKPISECKILLIDLSLDPERPSLEI 331
QY 268 MKDVESEVSPITPTFKPASLFSSSLRCADLTLPEDISOLCNDINDYAEVY 327
DB 332 M-DYVWERGT--PPSPITVMSSEAPNFD--IPF----- 361
QY 328 LMCTAGHLEKELYNKELIRSKPPICLTPNPLFEDGESFGQGRDSSLDDTDTTSLICQ 387
DB 362 -----EGSIVN-----FKMKCKSLILSMSSDKIQBQ 389
QY 388 LNRKLDVGEAEFPLEDDQSN--LPHSNNSNELSAATLPIILEKDTIYO--LNR1 442
DB 390 KRDYISSI--KSSIDKLEEVNQNRPLPHS-----LSPGTRKQYKRVVDIEAORLNDL 442
QY 443 ILPRLLRKAYP--YKKNDIWEKARVDIPPL-MRGITMAALLGYNAIHAHVDAIDKQTP1 499
DB 443 AREARIRRAQAVIRKELIATSTVNIKSEISLRILASCHLLTAKIVEA--EAQYKKGCL 500
QY 500 PTDR--QLE-----VDIPRCHQYDELLSSPGHAKFR--VLKA-----WVVSHP 540
DB 501 PKSRIPKIKHMIVTKWVDYSNKKGPSVOLSTEDIGVLFNNGTVLRLADEFWYIATSD 560
QY 541 DLVYWGQIDSLCAPFLVLTNNFNNALAVACMSAETPKYL-----YNFLKDNQSVI0HYL 594
DB 541 DREGW----VASHYVLTSEKPRELSRHLFVYDFEAKYMKAMISVSTFCREYHSDVPL 615
QY 595 TVFSQMIATFHPDPLSNHNLNIGLIPDLY--ALPWFIMFTVPLRK 639
DB 616 KRITRYKFFVWFELSDGTFQNF-KDHKKMAISDGKALVIYISPSHE 661

RESULT 12
CNK_MOUSE STANDARD: PRT: 631 AA.
ID CNK_MOUSE
AC Q60806; Q60822; Q9K009;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cytochrome-inducible serine/threonine-protein kinase (EC 2.7.1.37) (FCF-
DE inducible kinase).
GN CNK OR FNK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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RA Ushiro H., Tsutsumi T., Suzuki K., Kayahara T., Nakano K.:
 RT "Molecular cloning and characterization of a novel Ste20-related
 RT protein kinase enriched in neurons and transporting epithelia.";
 RL Arch. Biochem. Biophys. 355:233-240(1998).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE=Pancreas;
 RX MEDLINE=20445994; PubMed=10990492;
 RA Miao N., Pang B., Sanchez R., Lydon J., Barker D., Pang K.:
 RT "Isolation and expression of PASK, a serine/threonine kinase, during
 RT rat embryonic development, with special emphasis on the pancreas.";
 RL J. Histochem. Cytochem. 48:1391-1400(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Insulinoma;
 RX MEDLINE=20438689; PubMed=10980603;
 RA Johnston A.M., Naselli G., Gomez L.J., Martin R.M., Harrison L.C.,
 RA de Aizpuru H.J.:
 RT "SPAK, a STE20/SPS1-related kinase that activates the p38 pathway.";
 RL Oncogene 19:4290-4297(2000).
 CC -1- FUNCTION: MAY ACT AS A MEDIATOR OF STRESS-ACTIVATED SIGNALS.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC AND NUCLEAR (WHEN CASPASE-
 CC CLEAVED) (PROBABLE).
 CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN TESTES FOLLOWED BY
 CC PANCREAS, KIDNEY, HEART AND BRAIN. NOT EXPRESSED IN SKELETAL
 CC MUSCLE, LIVER, LUNG AND SPLEEN.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED IN THE EARLY GUT AND PANCREATIC
 CC EPITHELIUM, AT E15 DAY LOCALIZED TO CELLS THAT WILL EVENTUALLY
 CC BECOME EXOCRINE, PANCREATIC EPITHELIUM AND DORSAL ROOT GANGLIA.
 CC MYOCARDIUM, PANCREATIC EPITHELIUM AND DORSAL ROOT GANGLIA.
 CC -1- DOMAIN: PAPA BOX (PROLINE-ALANINE REPEATS) MAY TARGET THE KINASE
 CC TO A SPECIFIC SUBCELLULAR LOCATION BY FACILITATING INTERACTION
 CC WITH INTRACELLULAR PROTEINS SUCH AS ACTIN OR ACTIN-LIKE PROTEINS.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC STE20 SUBFAMILY.
 CC -----
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 DR EMBL: D88190; BAA26000.1; -;
 DR EMBL: AF068261; AAC23501.1; -;
 DR EMBL: AF099990; AAC72239.1; -;
 DR HSSP: P00518; PPK.
 DR InterPro: IPR000719; Euk_Pkinase.
 DR InterPro: IPR002290; Ser_thr_Pkinase.
 DR InterPro: IPR001245; Tyr_Pkinase.
 DR Pfam: PF00069; pkinase.1.
 DR PRINTS: PR00109; TYRKINASE.
 DR SMART: SM00220; S_TKc.1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; FALSE_NEG.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP.1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM.1.
 KM Transferase: Serine/threonine-protein kinase; ATP-binding.
 FT DOMAIN 14 52 PPO/ALA-RICH.
 FT NP_BIND 72 346 PROTEIN KINASE.
 FT BINDING 78 86 ATP (BY SIMILARITY).
 FT ACT_SITE 101 201 ATP (BY SIMILARITY).
 FT ACT_SITE 201 201 BY SIMILARITY.
 FT DOMAIN 22 30 POLY-ALA.
 FT DOMAIN 369 375 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT SITE 396 400 CASPASE CLEAVAGE RELATED SITE.
 FT CONFLICT 11 11 V -> I (IN REF. 2).
 FT CONFLICT 253 253 M -> I (IN REF. 2).
 FT CONFLICT 403 403 E -> Q (IN REF. 2).
 SU SEQUENCE 553 AA; 60050 MW; 8HC145BAE6F90C8 CRC64;

Query Match

5.3%; Score 250; DB 1; Length 553;

Best Local Similarity 23.9%; Pred. No. 2e-09;
 Matches 118; Conservative 81; Mismatches 179; Indels 116; Gaps 20;
 OY 37 KILGFELLKTTTHPRICQYVDISRGKHEKLVVAEHCERLEULR-----ERK-pv 88
 DB 114 ELKEIQAMSGSHENNVVYTSFVVKDELWLMKLLSGSGMDIIRYINRGEKKNGL 173
 OY 89 SCSTYLCIAFEVLOGLVQWKNKGIVHRLSPHNLIDKKKHILAKGLYHMTAGDVD 148
 DB 174 EBAITATILKKVLEGLDYLRKNGQIHRDLKGNILLEGDSVQIADQVSAFLATGIVT 233
 OY 149 PP-----IGPVSIAPEVIAAGIPEKTDHMSKPKLPSPGKSWSLGILLFEIYGRK 202
 DB 234 RKKVKTFTVGTICMMAPEVMEQ--VRGDF-----KAMMSVGIATIELATGAA 280
 OY 203 LPQSLDISERKFKHLLTDCVDDTLIVAEHGLDITKELPETVIDLKNKLTTPSKRP 262
 DB 281 PYHKYPPKVL--MLTGNDDPTLTFTGEVRK---EMKKYKGSFRLSLTSLDKPKSRP 345
 OY 263 TPDELMDKRVSEVSPLETPPTKIASLSSSLKADLTLPEDISQLRKDI-----NNQY 417
 DB 336 TAAELDKKRPFRK-----AKNREYIIEKLI---ITRTVDQAKAKKVRVPSSGHL 383
 OY 318 AERSIEEYVYIWLCLAGSDLEKELYNKEIIRSKPPICTLPNLFIDGSPGGRSSLD 377
 DB 384 --HKEDGDWMS-----DDPMDEKS-----EEKA-AASQEKSPRVK 418
 OY 378 DTTVTLISCOYRNLKLDVGC--EAVYPLEDDQSNLPHSNNSNLSAATLPLITREKT 435
 DB 419 EENPEISV-----NAGGIPEQIOLSVHSDGCPANEDYRGPCA-VNLVRLUNS 469
 OY 436 EYQLMRI-----ILF-----DLKAVPYKKNQIMKEARVDIPLM 471
 DB 470 RKEIINDIRFEPLPGDTADGVSQELFSAGLVGDGHVIVIAANLK-----IYDDPRAL 522
 OY 472 RGLTWAALLGVEGA 485
 DB 523 KLTFRKLASGCGGA 536
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 ID PLOT_SCHPO STANDARD: PRT: 683 AA.
 AC P50528;
 DT 01-OCT-1996 (rel. 34, Last sequence update)
 DT 01-OCT-1996 (rel. 34, Last sequence update)
 DT 16-OCT-2001 (rel. 40, Last annotation update)
 DE Serine/threonine-protein kinase p101 (Ec 2.7.1.1).
 GN P101 OR SPAC23C11.16.
 OS Schizosaccharomyces pombe (fission yeast).
 OC Schizosaccharomycetes; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-972;
 RX MEDLINE=95262899; PubMed=7744248;
 RA Ohkura H., Hagan J.M., Glover D.M.:
 RT "The conserved Schizosaccharomyces pombe kinase p101, required to
 RT form a bipolar spindle, the actin ring, and septum, can drive septum
 RT formation in G1 and G2 cells.";
 RL Genes Dev. 9:1059-1073(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-972;
 RA Brown D., Churcher C.M., Barrell B.G., Rajandream M.A., Wood V.:
 RL Submitted (Aug-1997) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: REQUIRED TO FORM A BIPOLAR SPINDLE. THE ACTIN RING AND
 CC SEPTUM, FUNCTIONS UPSTREAM OF THE WHOLE SEPTUM FORMATION PATHWAY,
 CC INCLUDING ACTIN RING FORMATION (REGULATED BY LATE SEPTATION GENES)
 CC AND SEPTAL MATERIAL DEPOSITION (REGULATED BY EARLY SEPTATION
 CC GENES). BEHAVES AS A "SEPTUM-PROMOTING FACTOR", AND COULD ALSO BE

Search completed: August 12, 2002, 09:12:35
Job time: 487 sec

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RESULT 3
ID AAF58257 standard: DNA: 936 BP.
XX
AC AAF58257:
XX
DI 24-APR-2001 (first entry)
XX
DE oligonucleotide D1954.
XX
KM Electron-transfer group: ETM; mismatch: genotyping:
XX
KM gene expression: ss.
XX
OS Synthetic.
XX
PN WC200107665-AZ.
XX
PD 01-FEB-2001.
XX
PF 26-JUL-2000; 2000WC-0520476.
XX
PR 26-JUL-1999; 990S-0145695.
XX
PR 17-MAR-2000; 2000US-0190259.
XX
PA (CLIN-) CLINICAL MICRO SENSORS INC.
XX
PI time RM:
XX
DR WPI: 2001-159728/16.
XX
PI Nucleic acids containing electron-transfer group, useful as labels in
PT hybridization assays, e.g. for genotyping, allowing repeat analyses on
PT a single surface.
XX
PS Example 6; Page 127; 159pp; English.
CC The present invention relates to a composition comprising two nucleic
CC acids each containing an electron transfer group (ETM) having
CC different redox potentials. The invention is used for electronic
```

CC detection of nucleic acids, especially of substitutions (mismatches)
CC and single-nucleotide polymorphisms, e.g. for genotyping.

CC monitoring gene expression.

XX
SO Sequence 936 BP; 5 A; 142 C; 7 G; 6 T; 776 other;

Query Match 4.38; Score 114; DB 22; Length 936;
Best local similarity 1.18; pred No 7.1e-23;

Matches 9; Conservative 477; Mismatches 302; Indels 0; Gaps 0;

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QY 806 aagacaaatallcaqlaagatatacattlataaccccttlaaccaactgacac 865
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QY 866 tcttccatctctctgagatgctgatttaactctgcttaagatatacattat 925
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1b 361 www.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww.ww 420
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RESULT 4
ID AAF58259
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AC AAF58259;
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[illegible][illegible]

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24 303 LERKENDSLPP-SQNTSELN 324
25 RESULT 2
26 US-08-893-274-10
27 Sequence 10, Application US/08893274
28 Patent No. 5968821
29 GENERAL INFORMATION:
30 APPLICANT: Beach, David H.
31 APPLICANT: Demetrick, Douglas J.
32 APPLICANT: Serrano, Manuel
33 APPLICANT: Hammon, Gregory J.
34 TITLE OF INVENTION: Cell Cycle Regulatory Proteins,
35 NUMBER OF INVENTION: and Uses Related Thereto
36 CORRESPONDENCE ADDRESS:
37 ADDRESSER: Policy, Board & Elliot LLP
38 STREET: One Post Office Square
39 CITY: Boston
40 STATE: MA
41 COUNTRY: USA
42 ZITE: 02109
43 COMPUTER READABLE FORM:
44 MEDIUM TYPE: Floppy disk
45 OPERATING SYSTEM: PC-DOS/MS-DOS
46 SOFTWARE: ASCII(LOCK)
47 CURRENT APPLICATION DATA:
48 APPLICATION NUMBER: US/08/893,274
49 FILING DATE: 15 JULY 1997
50 CLASSIFICATION: B00
51 PRIOR APPLICATION DATA:
52 APPLICATION NUMBER: US 08/606,511
53 FILING DATE: 14 SEPTEMBER 1994
54 PRIOR APPLICATION DATA:
55 APPLICATION NUMBER: US 08/248,812
56 FILING DATE: 25 MAY 1994
57 PRIOR APPLICATION DATA:
58 APPLICATION NUMBER: US 08/227,371
59 FILING DATE: 14 APRIL 1994
60 PRIOR APPLICATION DATA:
61 APPLICATION NUMBER: US 08/154,915
62 FILING DATE: 18 NOVEMBER 1993
63 PRIOR APPLICATION DATA:
64 APPLICATION NUMBER: US 07/991,997
65 FILING DATE: 17 DECEMBER 1992
66 PRIOR APPLICATION DATA:
67 APPLICATION NUMBER: US 07/964,408
68 FILING DATE: 16 OCTOBER 1992
69 ATTORNEY/AGENT INFORMATION:
70 NAME: Vignoli, Matthew P.
71 REGISTRATION NUMBER: 36,709
72 REFERENCE/MARKET NUMBER: MIV 071.09

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1 TELECOMMUNICATION INFORMATION:
2 TELEPHONE: (617) 832-7000
3 TELEFAX: (617) 832-7000
4 INFORMATION FOR SEQ ID NO: 10:
5 SEQUENCE CHARACTERISTICS:
6 LENGTH: 326 amino acids
7 TYPE: amino acid
8 MOLECULE TYPE: protein
9 FRAGMENT TYPE: N-terminal
10 US-08-893-274-10
11 Query Match 5.6%; Score 265; D8 2; Length 326;
12 Best Local Similarity 29.0%; Pred. No. 2,78-18;
13 Matches 94; Conserved Ipe 49; Mismatches 97; Indels 84; Gaps 16;
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22 167 ARI YSCWALTSVVVTLWRAPEVLQSSVAT PV-----DLSWVG 206
23 192 LLEFVWKRFLP-SLISEKRLTLQVVDPLVLAERGLDT----- 248
24 207 CTFAMERKRLPFRSSVVDQJLKI-----DVGLQGERHMPRVVALPQAFHSKSA 259
25 219 IKELFTVLDLNG-LTFHRSKRLPTDMLKDKVFSVSPLYPTPKPASFSS 292
26 260 QPIKEFVTDIDELCKDLKLCTFNPKR-----LSVSAISHY-----FQD 302
27
28 293 SLRC ADLLEPDIQJCKDIN 313
29 303 LERKENDSLPP-SQNTSELN 324
30
31 RESULT 1
32 US-08-581-918A-10
33 Sequence 10, Application US/08581918A
34 Patent No. 6043030
35 GENERAL INFORMATION:
36 APPLICANT: Beach, David H.
37 APPLICANT: Demetrick, Douglas J.
38 APPLICANT: Serrano, Manuel
39 APPLICANT: Hammon, Gregory J.
40 TITLE OF INVENTION: Cell Cycle Regulatory Proteins, and Uses
41 NUMBER OF SEQUENCES: 39
42 CORRESPONDENCE ADDRESS:
43 ADDRESSER: Policy, Board & Elliot
44 STREET: One Post Office Square
45 CITY: Boston
46 STATE: MA
47 COUNTRY: USA
48 ZITE: 02109
49 COMPUTER READABLE FORM:
50 MEDIUM TYPE: Floppy disk
51 OPERATING SYSTEM: PC-DOS/MS-DOS
52 SOFTWARE: Wordpad
53 CURRENT APPLICATION DATA:
54 APPLICATION NUMBER: US/08/581,918A
55 FILING DATE: 02-JAN-1996
56 CLASSIFICATION: 435
57 PRIOR APPLICATION DATA:
58 APPLICATION NUMBER: US 08/497,214
59 FILING DATE: 30 JUN-1995

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Tue Jun 26 08:50:48 2001

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Page 4

DB 240 GTEKEVTDIDELGKLLKLTFFNPAK 1SAVSA/SHIP 402
UY 293 SLRG ADTLEPDISQKODIN 413
DB 403 LERKRENDISHIP SONTSEIN 424

RESULT 5

US 08 842 946 10
Sequence 10, Application US/08842946
Patent No. 644575
GENERAL INFORMATION:
APPLICANT: MASSACHUSETTS
APPLICANT: ROBERTS, James M.
APPLICANT: KOLLY, Andrew
TITLE OF INVENTION: Isolated p27 Protein, Nucleic Acid
TITLE OF INVENTION: Methods of Identifying Agents Acting
NUMBER OF SEQUENCES: 10
ADDRESS/AGENT ADDRESS:
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZLN: 02109 2170
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: PLOTTER RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08842 946
FILING DATE: 21 FEBRUARY 1997
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 46,709
REFERENCE/AGENT NUMBER: MIV 079,05
TELEPHONE INFORMATION:
TELEPHONE: (617) 842 1000
TELEFAX: (617) 842 7000
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 426 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: N-terminal
US 08 842 946 10

Query Match 5.48; Score 254; DB 4; Length 426;

Host Local Similarity 28.78; Pctd No. 4.4e-17;

Matches 94; Conservative 48; Mismatches 99; Indels 84; Gaps 16;

UY 25 GSNGLPLTPNSKIKLGFUJTKITTPRGQYVD---ISKRIE RLVVVAEHCERSELD 80
DB 50 GECRMLP-STIREVAVLRLETFEHNVRKIDVCTVSRDRETKLTIVFXVXODLT 107
UY 81 LURERKPVVSCSVIAGFVAGIOLYMNKRGIVHRAISPHNILLDRKHILAKPGI 137
DB 108 YL DKVEPQVPTETIKDMFOLRLDLSHRVVRDLKPNILVTSSGQIKLADPGL 166
UY 138 YHMTAGDDVDVPIGYNS YLAEVLAGTIFKTDHMSKRPDPSGKSNVWSAG 191
DB 167 AKI YSPOMALISVAVILMYKAPVILQSSVAT PV-----DIMSWG 206
UY 192 ILLELVVGRKLFQSLDISERKFLTLKVGOTLIVAEHGGTLI----- 248
DB 207 CTFAEMRKRKTLERSSDVQJCKLT DVGLGHEHMDPRVVALPQAFHSKSA 259
UY 249 IKELFETVDIDELGKLLKLTFFNPAK-----ISAVSA/SHIP 292

DB 240 GTEKEVTDIDELGKLLKLTFFNPAK 1SAVSA/SHIP 402
UY 293 SLRG ADTLEPDISQKODIN 413
DB 403 LERKRENDISHIP SONTSEIN 424

RESULT 6

PCT/US95 04646-10
Sequence 10, Application PCT/US9504646
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
NUMBER OF SEQUENCES: 10
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(1981)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04646
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/446,147
FILING DATE: 29-NOV-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/406,511
FILING DATE: 14-SEP-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/248,812
FILING DATE: 25-MAY-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/227,471
FILING DATE: 14-APR-1994
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 426 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: N-terminal
PCT-US95-04646-10

Query Match 5.48; Score 253; DB 5; Length 426;

Host Local Similarity 28.78; Pctd No. 4.4e-17;

Matches 93; Conservative 48; Mismatches 99; Indels 84; Gaps 16;

UY 25 GSNGLPLTPNSKIKLGFUJTKITTPRGQYVD---ISKRIE RLVVVAEHCERSELD 80
DB 50 GECRMLP-STIREVAVLRLETFEHNVRKIDVCTVSRDRETKLTIVFXVXODLT 107
UY 81 LURERKPVVSCSVIAGFVAGIOLYMNKRGIVHRAISPHNILLDRKHILAKPGI 137
DB 108 YL DKVEPQVPTETIKDMFOLRLDLSHRVVRDLKPNILVTSSGQIKLADPGL 166
UY 138 YHMTAGDDVDVPIGYNS YLAEVLAGTIFKTDHMSKRPDPSGKSNVWSAG 191
DB 167 AKI YSPOMALISVAVILMYKAPVILQSSVAT PV-----DIMSWG 206
UY 192 ILLELVVGRKLFQSLDISERKFLTLKVGOTLIVAEHGGTLI----- 248
DB 207 CTFAEMRKRKTLERSSDVQJCKLT DVGLGHEHMDPRVVALPQAFHSKSA 259
UY 249 IKELFETVDIDELGKLLKLTFFNPAK-----ISAVSA/SHIP 292

Db 103 LERKENLDSHLP--SONTSELN 324

RESULT 7

US-07-857-224B-25

: Sequence 25, Application US/07857224B

: Patent No. 5958784

: GENERAL INFORMATION:

: APPLICANT: Bennett, Steven A.

: TITLE OF INVENTION: Predicting folded structures of proteins

: NUMBER OF SEQUENCES: 114

: CORRESPONDENCE ADDRESS:

: ADDRESSEE: Steven A. Bennett

: STREET: Hadlaubstrasse 151

: CITY: Zurich

: STATE: none

: COUNTRY: Switzerland

: ZIP: (note: this is an international post code) CH-8092

: COMPUTER READABLE FORM:

: MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage

: COMPUTER: Apple Macintosh

: OPERATING SYSTEM: Macintosh 7.0

: SOFTWARE: Microsoft Word

: CURRENT APPLICATION DATA:

: APPLICATION NUMBER: US/07/857,224B

: FILING DATE: 03/25/92

: CLASSIFICATION: 436

: PRIOR APPLICATION DATA: none

: TELECOMMUNICATION INFORMATION:

: TELEPHONE: (international) 41 1 632 2830

: TELEFAX: (international) 41 1 262 2437

: TELEX: none

: INFORMATION FOR SEQ ID NO: 25:

: SEQUENCE CHARACTERISTICS:

: LENGTH: 257

: TYPE: amino acid

: TOPOLOGY: linear

: MOLECULE TYPE: protein

: ORIGINAL SOURCE:

: ORGANISM: Saccharomyces cerevisiae

: FEATURE: Protein Kinase; Table 8 Column 28

: PUBLICATION INFORMATION:

: AUTHORS:

: AUTHORS: Hanks, S. K.

: AUTHORS: Hunter, J.

: TITLE: The protein kinase family

: JOURNAL: Science

: VOLUME: 241

: PAGES: 42-52

: DATE: 1988

: US-07-857-224B-25

Query Match 5.3%; Score 252.5; DB 2; Length 257;

Host local similarity 27.7%; Pred. No. 3.3e-17;

Matches 64; Conservative 50; Mismatches 84; Indels 33; Gaps 5;

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QY 45 LKTHPRLCGYVDISRKHERLVVAHCHERSLEDLREKRPVSCSTVLTAFEVIGSL 104
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 55 LELLNPHILIKLYDVTKSKDE-IIMVIEVANSLEFDYIVQRKMSQEARRFQUTISAV 113
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 105 CYMNHGIVHRAISPHNILLIKKKGRIKAKGCLYMTAHGIDVDPICVPSLAIEVIAO 164
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 114 ECHHKKIVHRLKPEMLLEHLNWKIADGLSNIMTDGMLTKTSGSPNYAAFEVIGSL 173
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 165 GIFTDIMPSSKPLSPSPKSDVMSGLIIFELGVGRKLFGLDISERKFLILLDCYDD 224
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 174 KLY-----AGRPVWVMSGVILYV-----ICKRLP-----DDE 203
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 225 TLIVLAE--EHGGLDIKELPETYDLNKKLTIFPSPKRPDPDELMKKVF 273
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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Db 204 SIPLPFNISNGVYTLPLKFLSPGASGLIKMLIVNPLNLSIHEIMDDMF 254

RESULT 8

US-08-878-989-15

: Sequence 15, Application US/08878989

: Patent No. 5885803

: GENERAL INFORMATION:

: APPLICANT: Handman, Olga

: APPLICANT: Hillman, Jennifer L.

: APPLICANT: Cortley, Neil C.

: APPLICANT: Guegler, Karl G.

: APPLICANT: Lal, Preeli

: APPLICANT: Goli, Surya K.

: APPLICANT: Shah, Purni

: TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN

: TITLE OF INVENTION: KINASES

: NUMBER OF SEQUENCES: 21

: CORRESPONDENCE ADDRESS:

: ADDRESSEE: Incyte Pharmaceuticals, Inc.

: STREET: 3174 Porter Drive

: CITY: Palo Alto

: STATE: CA

: COUNTRY: USA

: ZIP: 94304

: COMPUTER READABLE FORM:

: MEDIUM TYPE: Diskette

: COMPUTER: IBM Compatible

: OPERATING SYSTEM: DOS

: SOFTWARE: FastSeq for Windows Version 2.0

: CURRENT APPLICATION DATA:

: APPLICATION NUMBER: US/08/878,989

: FILING DATE:

: CLASSIFICATION: 435

: PRIOR APPLICATION DATA:

: APPLICATION NUMBER:

: FILING DATE:

: ATTORNEY/AGENT INFORMATION:

: NAME: Billings, Lucy J J

: REGISTRATION NUMBER: 16,749

: REFERENCE/DOCKET NUMBER: PP-0321 US

: TELECOMMUNICATION INFORMATION:

: TELEPHONE: 415-855-0555

: TELEFAX: 415-845-4166

: TELEX:

: INFORMATION FOR SEQ ID NO: 15:

: SEQUENCE CHARACTERISTICS:

: LENGTH: 607 amino acids

: TYPE: amino acid

: STRANDEDNESS: single

: TOPOLOGY: linear

: IMMEDIATE SOURCE:

: LIBRARY: Genbank

: CLONE: 1827450

: US-08-878-989-15

Query Match 5.2%; Score 247.5; DB 2; Length 607;

Host local similarity 24.0%; Pred. No. 4.9e-16;

Matches 107; Conservative 69; Mismatches 163; Indels 107; Gaps 18;

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QY 35 SIKLIGROIILKTIHPRLCYVDISRK-KHERLVVAERFE-----RSLE 79
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 50 AVKVIPOSVAKKPHQREKILNFTLHRLQHRHIVKPSHREDADNIVYILELCSKSLA 109
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 80 DLREKRPVSCSTVLCTAFEVIGSLGYMNHGIVHRAISPHNILLDRKGRIKAKFGLYH 139
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 110 HIMARHITLLEPEVRYVYIQLTSLGKLYLHGSLHRLDKLGNFTITENMELKVGDFDLA 169
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 140 MTAHGIDVDPICVPSLAIEV--IAOGIFKTTIHMSKKPLNSGPKSDVMSGLIIFEL 197
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 170 RLEPEURKKTIGTIPNVAAFEVILRQ-----HGPPADVMSLGVVYTL 214
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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07 198 CVCGRKLPQSDLSIRKRLKLTLLVADLVLAERHGTDLIKELPEVLDLANKLTPH 257
10 215 LQSPPEIADLKE-----TYGCI-----KQVHTPLVASLSLPAR-QLLAAILRAS 259
09 258 PSKRPTPEELMKDKVESEVSPLYPTFTKPAFLSSSLRCADLTLPEDISQLC 309
10 260 PROPKSTIDQTLRHDPFRK---YTPDRLP---ISSCYVVDLTPPNANRSLFAAVTSKLP 313
07 410 KQINDNYLAERSTEEVYVLMGLAGDELEKELVNEKELIRSKPTCTLP----- 356
10 414 GRKKRSKNHAQER-DEVSGL-VSG-LMRTSVHQDARPEAPVAPASVEAVSEVETAFE 367
07 457 NLFPEDESGPGGRKRSLLDITVTLSTQVLRNRLKQVGGAPVPLLEDQSNL 411
10 468 LSSPRGTIASSGGFEFG-----LTVAIVESA/CALRNC1-----APMPAEONAPL 416
07 412 PHSNSNELSAATLELTIREKDEY 437
10 417 -----AOPPELVWVSKWVY 431

```

```

RESULT 9
US 09 272 796 15
Sequence 15, Application US/09272796
Patient No. 6207148
GENERAL INFORMATION:
APPLICANT: Beaudoin, Claude
APPLICANT: Bellemare, Penelope L.
APPLICANT: Guelley, Noelle C.
APPLICANT: Guelley, Karl G.
APPLICANT: Lall, Pierre
APPLICANT: Gault, Sotya K.
TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
TITLE OF INVENTION: KINASES
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESS: Incyte Pharmaceuticals, Inc.
STREET: 4174 Port of Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09272796
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/878,989
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.J.
REGISTRATION NUMBER: 46,749
REFERENCE/DOCKET NUMBER: PC 0121 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415 845 0555
TELEFAX: 415 845 4166
TELEX:
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 407 amino acids
TYPE: amino acid
SUBSTANCE: Stride
IMMEDIATE SOURCE:
LIBRARY: Genbank
CLONE: 1827450
US 09 272 796 15

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Query Match 5.2%; Score 247.5; 108 4; Length 607;
Best Local Similarity 24.0%; Pred. No. 4,96-16;
Matches 107; Conserved 69; Mismatches 163; Indels 107; Gaps 18;
07 45 SIKLCPQVLLKTLIRLCQVYVLSNG-KHKKLVVAER-----RSLE 79
10 50 AVKVPQSRVAKPRQKRLINLEIHDLDQRIIVRESHMEEDADNYIFELGSKSLA 109
07 80 DLPERKVASSTVGLAIFVLOGVYNNKHGIVHVALSPNILLRKHIIKLAKGLTH 139
10 110 HMKARHILLPEPKRYVLRQVLSKTLHQRGLHRLKIGNFTTNMELKVGQDLAA 169
07 140 MIAQGVDEPI-GYSPYLAPEV-IAQGIKRTTDMESKKPLPSGKSGVWSGIIIFEL 197
10 170 KLEPPEQRKKTIGTPVYVAPEVILRQ-----HPEAVWSGQVWYTL 214
07 198 CVCGRKLPQSDLSIRKRLKLTLLVADLVLAERHGTDLIKELPEVLDLANKLTPH 257
10 215 LQSPPEIADLKE-----TYGCI-----KQVHTPLVASLSLPAR-QLLAAILRAS 259
07 258 PSKRPTPEELMKDKVESEVSPLYPTFTKPAFLSSSLRCADLTLPEDISQLC 309
10 260 PROPKSTIDQTLRHDPFRK---YTPDRLP---ISSCYVVDLTPPNANRSLFAAVTSKLP 313
07 410 -KQINDNYLAERSTEEVYVLMGLAGDELEKELVNEKELIRSKPTCTLP----- 356
10 414 GRKKRSKNHAQER-DEVSGL-VSG-LMRTSVHQDARPEAPVAPASVEAVSEVETAFE 367
07 457 NLFPEDESGPGGRKRSLLDITVTLSTQVLRNRLKQVGGAPVPLLEDQSNL 411
10 468 LSSPRGTIASSGGFEFG-----LTVAIVESA/CALRNC1-----APMPAEONAPL 416
07 412 PHSNSNELSAATLELTIREKDEY 437
10 417 -----AOPPELVWVSKWVY 431

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RESULT 10
US 08 252 995D-14
Sequence 13, Application US/08252995D
Patient No. 5650501
GENERAL INFORMATION:
APPLICANT: Dennis, James W
APPLICANT: Bellemare, Mike
APPLICANT: Fode, Carol
TITLE OF INVENTION: NOVEL SPRING/PHOSPHINE KINASE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESS: BERESKIN & PARK
STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATGUT to Release #1.0, Version #1.10
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/252,995D
FILING DATE: 02-20-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Korydyk, Linda M.
REGISTRATION NUMBER: 34,971
REFERENCE/DOCKET NUMBER: 3153-96
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 464-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 13:

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1  APPLICANT: Nakano, Takeshi
2  APPLICANT: Ito, Masaaki
3  APPLICANT: Takahashi, No. 5906819uaki
4  TITLE OF INVENTION: RHO TARGET PROTEIN RHO-KINASE
5  NUMBER OF SEQUENCES: 16
6  CORRESPONDENCE ADDRESS:
7  ADDRESSEE: Policy & Lardner
8  STREET: 3000 K Street, N.W., Suite 500
9  CITY: Washington
10 STATE: D.C.
11 COUNTRY: USA
12 ZIP: 20007-5109
13 COMPUTER READABLE FORM:
14 MEDIUM TYPE: Floppy disk
15 COMPUTER: IBM PC compatible
16 OPERATING SYSTEM: PC-DOS/MS-DOS
17 SOFTWARE: Patent In Release #1.0, Version #1.30
18 CURRENT APPLICATION DATA:
19 APPLICATION NUMBER: US
20 FILING DATE: 24-JUL-1996
21 CLASSIFICATION: 435
22 PRIOR APPLICATION DATA:
23 APPLICATION NUMBER: JP 7-425129
24 FILING DATE: 20-NOV-1995
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER: JP 8-17150
27 FILING DATE: 05-JAN-1996
28 PRIOR APPLICATION DATA:
29 APPLICATION NUMBER: JP 8-11206
30 FILING DATE: 26-APR-1996
31 ATTORNEY/AGENT INFORMATION:
32 NAME: Reule, Stephen A.
33 REGISTRATION NUMBER: 29,768
34 REFERENCE/PACKET NUMBER: 16887/843
35 TELECOMMUNICATION INFORMATION:
36 TELEPHONE: (202)672-5300
37 TELEFAX: (202)672-5399
38 TELEX: 904136
39 INFORMATION FOR SEQ ID NO: 5:
40 SEQUENCE CHARACTERISTICS:
41 LENGTH: 4563 base pairs
42 TYPE: nucleic acid
43 STRANDEDNESS: single
44 TOPOLOGY: linear
45 MOLECULE TYPE: cDNA
46 ORIGINAL SOURCE:
47 ORGANISM: Homo sapiens
48 FEATURE:
49 NAME/KEY: CDS
50 LOCATION: 1..4164
51 OS-08-685-576-5

```

RESULT 5
US-08-557-006C-48
; Sequence 38, Application US/08557006C

1 Patent No. 5,259,547
 2 GENERAL INFORMATION:
 3 APPLICANT: Hoff, Rajinder K.
 4 APPLICANT: Carling, David
 5 APPLICANT: Forde, Robert A.
 6 TITLE OF INVENTION: NUCLEIC ACID ENCODING AMP-ACTIVATED PROTEIN KINASE
 7 FILE REFERENCE: NCAM/PHK37588/UST
 8 CURRENT APPLICATION NUMBER: US/08/557, 006C
 9 PRIOR FILING DATE: 1996-03-06
 10 PRIOR APPLICATION NUMBER: PCT/GB94/01093
 11 PRIOR FILING DATE: 1994-05-20
 12 PRIOR APPLICATION NUMBER: GB 9410489.1
 13 PRIOR FILING DATE: 1993-05-21
 14 PRIOR APPLICATION NUMBER: GB 931010.7
 15 PRIOR FILING DATE: 1993-08-31
 16 NUMBER OF SEQ ID NOS: 44
 17 SOFTWARE: PatentIn Ver. 2.1
 18 SEQ ID NO: 38
 19 LENGTH: 1742
 20 TYPE: DNA
 21 ORGANISM: Human AMP protein kinase
 22 US-08-557-006C-38

```

Query Match 1.68; Score 42; 38 4; Length 1742;
Best Local Similarity 51.08; Pred. No. 0.017;
Matches 99; Conservative 0; Mismatches 95; Indels 0; Gaps

OY 296 aggtcttcaaggtcttcaagtatatataaacaacatgatatagatcaacaggaatctctc 455
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 365 agattctctctctctctctgaactaactctgtcttcacagacaaagttcttcctaaaggaacttgaa 424
OY 356 ctcatataatctctatgacccggaagaacataataataattgctlaatttgactttatc 415
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 425 cagaagaagatctgtctgacagcccaagatgatgtaagaataactgacttccgaactctcta 484
OY 416 acatgacagctctcatgcatgataatttatttctccataagatctccctactatgcc 475
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 485 atatgattctgacatgtcaattctctacgaactaactgtgagatctcgaataattatgcacac 544
OY 476 ctgaggaattatga 489
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 545 cagaagctatcttca 558

RESULT 6
1 Sequence 39; Application US/08557006C
2 Patent No. 6258547
3 GENERAL INFORMATION:
4 APPLICANT: Bcrf, Rajindar K.
5 APPLICANT: Carling, David
6 APPLICANT: Pordorf, Robert A.
7 TITLE OF INVENTION: NUCLEIC ACID ENCODING AMP-ACTIVATED PROTEIN KINASE
8 FILE REFERENCE: NGAP/PHM37588/UST
9 CURRENT APPLICATION NUMBER: US/08/557,006C
10 CURRENT FILING DATE: 1996-03-06
11 PRIOR APPLICATION NUMBER: PCT/GB94/01093
12 PRIOR FILING DATE: 1994-05-20
13 PRIOR APPLICATION NUMBER: GB 9310489.1
14 PRIOR FILING DATE: 1994-05-21
15 PRIOR APPLICATION NUMBER: GB 9318010.7
16 PRIOR FILING DATE: 1993-08-31
17 NUMBER OF SEQ ID NOS: 44
18 SOFTWARE: PatentIn Ver. 2.1
19 SEQ ID NO 39
20 LENGTH: 2652
21 TYPE: DNA
22 ORGANISM: Rat
23 FEATURE:
24 NAME/KEY: gene
25 LOCATION: (1)..(1747)
26 OTHER INFORMATION: Full length cDNA sequence fragment of Human AMPK -

```


Db 648 GCGTCGTAATGATGCTCTTGTGATTAACATGCGCATCTAAATTAGCAGATTTCGCATG 707

QY 414 TCAATGACACCTCA 428
Db 708 TATGAAATGATGATCA 722

RESULT 9

US-08-860-150-6
Sequence 6, Application US/0860150B
Patent No. 5981205
GENERAL INFORMATION:
APPLICANT: Hemmings, Brian A.
APPLICANT: Millward, Thomas A.
TITLE OF INVENTION: Nuclear DBF2-Related (NDR) Kinases
FILE REFERENCE: 4-20265/A/PCT
CURRENT APPLICATION NUMBER: US/08/860,150B
CURRENT FILING DATE: 1997-06-19
EARLIER APPLICATION NUMBER: PCT/EP95/05052
EARLIER FILING DATE: 1995-12-20
EARLIER APPLICATION NUMBER: 94810746.1
EARLIER FILING DATE: 1994-12-22
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 4018
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (596)..(1990)
US-08-860-150-6

Query Match 1.5%: Score 40.4; DB 2; Length 3018;
Best Local Similarity 61.3%: Pred. No. 0.07;
Matches 65; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 307 qacttgcagatatacaacaacatgataatgacacagagcattgtctccataataac 366
Db 1190 gccatagacactatctaccacacttgaattatccacagagacatcaaccagacacct 1249

QY 367 ctgttgcacccaaagacacataaattggcctaattgacctt 412
Db 1250 cttttgacacagacacatgtaaaccttctgacctttt 1295

RESULT 10

US-09-338-132-6
Sequence 6, Application US/09338132
Patent No. 6040164
GENERAL INFORMATION:
APPLICANT: Hemmings, Brian A.
APPLICANT: Millward, Thomas A.
TITLE OF INVENTION: Nuclear DBF2-Related (NDR) Kinases
FILE REFERENCE: 4-20265/A/PCT
CURRENT APPLICATION NUMBER: US/09/338,132
CURRENT FILING DATE: 1999-06-22
EARLIER APPLICATION NUMBER: 08/860,150
EARLIER FILING DATE: 1997-06-19
EARLIER APPLICATION NUMBER: PCT/EP95/05052
EARLIER FILING DATE: 1995-12-20
EARLIER APPLICATION NUMBER: 94810746.1
EARLIER FILING DATE: 1994-12-22
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 3018
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS

LOCATION: (596)..(1990)
US-09-338-132-6

Query Match 1.5%: Score 40.4; DB 4; Length 3018;
Best Local Similarity 61.3%: Pred. No. 0.07;
Matches 65; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 307 qacttgcagatatacaacaacatgataatgacacagacattgtctccataataac 366
Db 1190 gccatagacactatctaccacacttgaattatccacagagacatcaaccagacacct 1249

QY 367 ctgttgcacccaaagacacataaattggcctaattgacctt 412
Db 1250 cttttgacacagacacatgtaaaccttctgacctttt 1295

RESULT 11

US-09-313-930-1
Sequence 1, Application US/09313930
Patent No. 625723
GENERAL INFORMATION:
APPLICANT: Dean, Nicholas M.
TITLE OF INVENTION: Antisense Oligonucleotide Modulation of Human Protein
FILE REFERENCE: ISPH-0357
CURRENT APPLICATION NUMBER: US/09/313,930
CURRENT FILING DATE: 1999-05-18
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 2104
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (59)..(2089)
PUBLICATION INFORMATION:

AUTHORS: Arts, J. P.
AUTHORS: Basta, P. V.
AUTHORS: Holmes, W. D.
AUTHORS: Holmes, L. M.
AUTHORS: Moosaw, C.
AUTHORS: Rankl, N. B.
AUTHORS: Blobel, G.
AUTHORS: Loomis, C. R.
AUTHORS: Burns, D. J.
TITLE: Molecular and biochemical characterization of a
TITLE: recombinant human PKC-delta family member
JOURNAL: Biochim. Biophys. Acta
VOLUME: 1174
ISSUE: 2
PAGES: 171-181
DATE: 1993-08-19
DATABASE ACCESSION NUMBER: U07860
DATABASE ENTRY DATE: 1993-11-02
US-09-313-930-1

Query Match 1.5%: Score 39.8; DB 4; Length 2104;
Best Local Similarity 56.5%: Pred. No. 0.085;
Matches 74; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 282 gttatagactttgaacttctgaacttgcagatatacaacaacatgataatgacac 341
Db 1411 gtttatgcctccgaataataatgtaactgacattctacacagaaagacatcatlta 1470

QY 342 caggacatgctccatcaataataatctgttgaacacaaagacataatgaactaa 403
Db 1471 caagacatcaaacctgacacataatgctgttgaacacaaagacataatgaactaa 1510

QY 402 atttgaactt 412
||||| |

GenCore version 4.5
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CM protein - protein search, using sw model

Run on: August 12, 2002, 08:03:28 ; Search time 42.77 Seconds
(without alignments)
2006.261 Million cell updates/sec

Title: US-09-707-121-2
Perfect score: 4721
Sequence: 1 MFPLKDAEMGATFFASALP.....DCGINKIKPTGLTIIPSPQI 893

Scoring table: BL0SUM62
Gapop 10.0 , Gapext 0.5

Searched: 28318 seqs, 9609334 residues

Total number of hits satisfying chosen parameters: 28318

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1.*
2: p1r2.*
3: p1r3.*
4: p1r4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	870	18.4	826	2	T15751
2	399.5	8.5	1784	2	T02844
3	280	5.9	1142	2	S59359
4	278	5.9	511	1	A56009
5	275	5.8	576	2	T41587
6	271	5.7	602	2	S72513
7	268	5.7	633	1	A26030
8	265.5	5.6	326	2	S23387
9	259	5.5	512	2	T52633
10	257	5.4	504	2	T10449
11	256.5	5.4	512	2	T07788
12	254.5	5.4	510	2	T04145
13	252	5.3	512	1	J01446
14	252	5.3	705	2	A48144
15	251.5	5.3	631	2	A57286
16	250	5.3	401	2	B90120
17	249.5	5.3	651	2	A46591
18	249	5.3	683	2	T38254
19	247	5.2	502	1	A41361
20	246.5	5.2	504	2	T07415
21	246	5.2	1192	2	T18611
22	246	5.2	1246	2	G89287
23	244	5.2	278	2	S46387
24	243.5	5.2	513	1	S60303
25	240.5	5.1	513	1	S60304
26	240	5.1	443	2	S59140
27	240	5.1	473	1	S59941
28	240	5.1	745	2	G01025
29	240	5.1	775	2	F38929

30	239	5.1	443	2	S38327	serine/threonine-s
31	238.5	5.1	372	2	S15663	protein kinase (b)
32	237.5	5.0	560	2	S51600	phosphorylase kina
33	237	5.0	887	2	T20941	hypothetical prote
34	235.5	5.0	713	2	S27966	probable serine/th
35	235	5.0	372	2	S39559	mitogen-activated
36	234.5	5.0	406	2	D84898	probable mitogen a
37	234.5	5.0	37	2	J07500	gik protein - chic
38	234	5.0	38	2	H90100	SNF-related kinase
39	233.5	4.9	562	2	T29858	hypothetical prote
40	233	4.9	371	2	S60121	mitogen activated
41	231.5	4.9	1062	2	S46367	protein kinase (p)
42	231	4.9	774	2	T48609	probable serine/th
43	231	4.9	1130	1	TVH0A	protein-tyrosine k
44	230.5	4.9	475	2	T12955	probable protein k
45	230.5	4.9	1001	2	T17365	serine/threonine p

ALIGNMENTS

RESULT 1
T15751
hypothetical protein C33F10.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T15751
K:Chisoe, S.
Submitted to the EMBL Data Library, February 1996
A:Description: The sequence of C. elegans cosmid C33F10.
A:Reference number: Z18397
A:Accession: T15751
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-826 <CH1>
A:Cross-references: EMBL:049830; NID:q1203933; PTD:q1203941; PIDN:AAA3369.1; CESP:C3
C:Genetics:
A:Gene: CESP:C33F10.2
A:Introns: 38/2; 62/1; 141/2; 193/3; 246/3; 384/3; 456/1; 547/1; 704/1; 742/2

Query Match	18.4%	Score 870;	DB 2;	Length 826;
Best Local Similarity	28.9%	Pred. No. 9.9e-39;		
Matches 265;	Conservative 138;	Mismatches 358;	Indels 156;	Gaps 27;
QY	2	FPLKDAEMGATFFASALPMDVCGSNGLPITWNSIKILGRPOLKTIHPRLOVYDYSR 61		
DB	4	FP---NFGAFILRAQEKDRTG-INGIPVAPAKOMIGRPVYLOSTQHUNLSVYLFSE 58		
QY	62	C-KHERLVVAHCEGSEHDLERRKPVSGSTVLCIAFVILGIVYNNKHGIVHRAISP 119		
DB	59	TVIARDLVIVMEHYTMLEDLITGNKDESLNNFYSELSALDYLIFRNIYHGLHL 118		
QY	120	HNILLDKKGH---IKIAFGIYHMTAGDVPDPICYPSTLAPEVI---AGGIFKTDH 172		
DB	119	NSIITIDKRNKGLSVKLSGVLPLVINGKPIASSJAFGAFIAFERILLINDEDSIFAAT-- 176		
QY	173	MPSKKPLPSGKRSVNSGILLFELCVGRKLPQSLDISERIKPL---LTLD-----CYD 223		
DB	177	-----YQSDVMEIASPILDIYIGISLEAVETFEYILEJNNKYIIDQERKISTYME 226		
QY	224	DTLVIAFEGHGLDIKELP-----EIVDILNLCIFPHSSKRPIDPELKKDKVFSVSP 274		
DB	227	DLIQLLADK-----KLPYHKKCEMLEATIRKGLQMKSKKSGITF-----VAALRI 274		
QY	279	LYPFTKVASLFSSSLKCAADLTLPEDISQICRDI--NNDIYLAERSIDPYYVLMCLAGDL 346		
DB	275	NINGVKNNNNKYYEKVK---TVEEMRAAVKAEVADNNDDEKELISVNSFYLMKTCGSP 330		
QY	337	EKEIVNKEIISKRPICITIPNFIFPDGFSFGQGRKSLID---DTIVITLSICOLKN 390		
DB	331	ELLKKKQIIONHAFISSYPIVREDDELRLDSQVNSISFEYGVFDLPSKKTITRKETGQ 390		

278 -----PLYPTETKPSLFFSSSLKCAADLT-----PEDISQCKDINDY 316
 296 RDSKRIKLPREDIYLTPLSSNSSI---DATILQNLVLMHGROPEIKERLPCAN- 351
 317 LAERSELEVYLLM-CLAGDLEKELVNEKIRSKRP-----CLTLPFLLEDGE 364
 352 -AEKTLVAILYHFKC---DTQKELIKQYQKKRQSSIVSSPSKVVSTTPQ----- 399
 365 SPQGGHDKSSLLDITVLLSLGULNNKIKDVGGEAFYPLLEDQSNLPHSNNELS 421
 400 ---RRKNRESLISVTS-----SRKKPISFNKF-TASSASSSNLTTPGSKRSL 443

RESULT 4

A56009
 serine/threonine-specific protein kinase (EC 2.7.1.-) NPK5 - common tobacco
 C:Species: Nicotiana tabacum (common tobacco)
 C:Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 16-Jun-2000
 C:Accession: A56009
 R:Murataka, T.; Hano, H.; Machida, Y.
 Mol. Cell. Biol. 14, 2958-2965, 1994
 A:Title: Characterization of tobacco protein kinase NPK5, a homolog of Saccharomyces cerevisiae of Saccharomyces cerevisiae.
 A:Reference number: A56009; MUID:94217693
 A:Accession: A56009
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-511 <MDR>
 A:Cross-references: DB:D26602; NID:q496384; PIDN:BA005649.1; PID:q496385
 C:Function:
 A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine
 C:Superfamily: AMP-activated protein kinase; protein kinase homology
 C:Keywords: ATP; magnesium; phosphotransferase; serine/threonine-specific protein kinase
 F:17-271/Domain: protein kinase homology <KIN>
 F:25-33/Region: protein kinase ATP-binding motif
 F:48-67/142,144/Active site: Lys, Glu, Asp, Lys #status predicted
 F:147/151/Binding site: magnesium (Asn, Asp) #status predicted

Query Match 5.98; Score 278; DB 1; Length 511;
 Best local similarity 21.0%; Pred. No. 1.3e-07;
 Matches 124; Conservative 84; Mismatches 184; Indels 198; Gaps 19;
 35 SIKILAR-----FOILKILTHPRLCYVDINSKGRHLVVAEHERSLE 79
 46 AVKILNRKIKKMEHEKVRKFKILRLPMRPHILRLVEVETPSDIYVMEYKSGELF 105
 80 DLIREKKVYSCSTVLCTAFEVIGLOVMKNGIHVRLSPHLLDRKGHLKLAKEGLYH 139
 106 DYIVKKGRIQHPARKKFRQJLISVEYCHRNMYVRDLKPHLLDSKMNKVIAPFGLSN 165
 140 MIAHGDDVDPIGYPSTLAPEVIAOGIEKTDHMPSKKRLNSGPKSDVWSLGIILFELCV 199
 166 IMRDGHFLKTSQSGSPNYAPEVINSGLY-----AGPEVDVWSGCVLIYALIC 212
 200 GKRLQSDISRLKFLITLDCVDTLLVLAHEHGLDILKLPETVIDLLNCKLTFHRS 259
 213 GILPDEDEMPILPKKI-----KGNISLPSHLSAGARLIPRMILVDPM 257
 260 KSPTEDELKMDKVFSEVSLYTPETKPSLSESSSLKCADLTPEDISQCKDINDYLAE 319
 258 KMTIPEIKMHMFQAHLPKYLAV-----PPTMQAKKIDEDIL-- 298
 320 KSTIEVYVIMLACGHLKEHLVNEKIRSKRPICITLPNLFEDGESFOGDRSSLLDIT 379
 299 -----QEVYK-----KGFDRNSLIV-- 312
 380 TITLSICQLRNLIKQVGFAPFLLEDQSNLPHSNNELSAANTPLIRKKTETVQL 439
 313 ---ASLC---NNVQNGIVAYVILF-----NPRASSQYKGAPEQETMEVGY 354
 440 NRIILFDRL-----KAYPYKKNOIW-----KEARVDIPILMR 472

355 HOINSSEVLLPCMOHLPGIMDFQVGARQFVERK--WALQDSRAIRPRIMTEIKALQ 412
 473 GLT--MAAL-----LQVEG-----AIHAAYDALDK-----DTPIPTDQIE 506
 413 GLNVKMKIGPYNNKQWMPGVPGNHGMSNNSIHIGFPGDDSTVIRNGCVTIPNAVKE 472
 507 VDIPIRGIDYDLSSPRGNKAFRVLKAMVVSIPDLVYMGDLSL/APFL 556
 473 VOLKTRKELTLDLR-----VQSGPFLF---ID-LTAAFL 505

RESULT 5

T41587
 probable carbon catabolite derepressing protein kinase - fission yeast (Schizosacchar
 C:Species: Schizosaccharomyces pombe
 C:Date: 03-Dec-1999 #sequence_revision 01-Dec-1999 #text_change 31-Jan-2000
 C:Accession: T41587
 R:Murphy, L.; Harris, D.; Iyne, M.; Rajandream, M.A.; Bartell, H.G.
 submitted to the FMRJ data library, September 1996
 A:Reference number: Z21968
 A:Accession: T41587
 A:Status: preliminary; translated from GI/FMN1/MDM1
 A:Molecule type: DNA
 A:Residues: 1-576 <MDR>
 A:Cross-references: EMBL:AL031543; PIDN:CA020833.1; GSPDB:GNO00068; SPDB:SPDC74.03C
 A:Experimental source: strain 972n; cosmid c74
 C:Genetics:
 A:Gene: SPDB:SPDC74.03C
 A:Map position: 3
 A:Inserts: 50/1; 127/3; 245/1
 C:Superfamily: AMP-activated protein kinase; protein kinase homology

Query Match 5.88; Score 275; DB 2; Length 576;
 Best local similarity 21.3%; Pred. No. 2.1e-07;
 Matches 122; Conservative 96; Mismatches 202; Indels 154; Gaps 21;
 45 LKTIHPRLCYVDINSKGRHLVVAEHERSLEDLIREKRVSCSTVLCTAFEVIGL 104
 86 LKLLRPHPTIKLVNVTTPD-IWVVIYAGGELDYIVKRRMTEDGRRFQVITCAL 144
 105 QYNNKGIHVRALSPHNLIDRKGHIKLAKGLYHMTANGDDVDPIGYPSTLAPEVIAO 164
 145 EYCHRRKIVHNDLPENLLDNNINVKIAPFGLSINIMTKNLFKTSQSGSPNYAPEVING 204
 165 GIEKTDHMPSKRPLSPKSDVWSLGIILFELCVGRKIFQSDISRLKFLITLDCVVD 224
 205 KLY-----AGPEVDVWSGCVLIYVMEVGRFLP-----DD 233
 225 TLI--VLAHEHGLDILKE-LPETVIDLLNCKLTFHRSKRTPEHLMKDKVFSVSPLYT 281
 224 FETPNLEKRVSCYVMPDFLSPGASQSLIRRIYADPRGRTIOELIRDDVFNFNITDY- 292
 282 PTKPSLSESSSLKCADLTPEDISQCKDINDYLAE-----RSTIEVYVIMLACG 344
 293 --LRMEVQGSY--ADSRIVSKIGF-AMGSPDYVIALKSDENNEKVAYNL----- 341
 335 DLKHLVNEKIRSKRPIC--TLPNF-----FEKESFGQGRKSSLLDIT----- 379
 342 ---LHNGVTOEKSLSKSRVDSFLVSAPFSEVTSLELOKKSQELIDPTLEGPBW 396
 360 -----TITLSICQL-----RNLIKQVGFAPYPLLEDQSNLPHSNNELSAA 423
 397 TVSDPPIYAKOTIDNSIGVILVPTAEKNKLE-----MTIADASAVITVSOTIRKSR 449
 424 ATPLIRKKTETVQNLILFDRLKAY-----PYKKNOIWKEARV 465
 450 NKMHGVGVRGQDAPRI-----LLAVYKALQAGAGFTYPKPVNKGKRSMDWTISRW 501
 466 DIPRLMGLTMAALCGVCAIHAKYDALDKTPIPTDQIEVDIPRGHVDIELSSPRGH 525
 502 EIP-----HCKREG--KNTIVATIELQLEVMPGCMAD--VKSNGY 538

EMBL J. 11, 2909-2917, 1992
 A:Title: A family of human cd2-related protein kinases.
 A:Reference number: S23382; MUID:92347325
 A:Accession: S23387
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-326 <ME>
 A:Cross-references: EMBL:X66365; NID:q36622; PIDN:CA47008.1; PID:q36623
 C:Genetics:
 A:Gene: GDB:CDK6
 A:Cross-references: GDB:283458
 A:Map position: 7q36-7q36
 C:Superfamily: kinase-related transforming protein; protein kinase homology
 C:Keywords: ATP; cell cycle control; phosphoprotein; phosphotransferase; serine/threonine
 F:11-284/Domain: protein kinase homology <KIN>
 F:19-27/Region: protein kinase ATP-binding motif
 F:24/Binding site: phosphate (tyr) (covalent) *status predicted
 F:43,61,145,147/Active site: lys, glu, asp, lys *status predicted
 F:177/Binding site: phosphate (thr) (covalent) *status predicted
 F:290/Binding site: phosphate (ser) (covalent) *status predicted

Query Match 5.6%; Score 266.5; DB 2; Length 326;
 Best Local Similarity 28.4%; Prod. No. 3e-07;
 Matches 99; Conservative 52; Mismatches 112; Indels 85; Gaps 17;
 QY 1 MPRLDAMGATFFASALPHDVGSGNGLPLTPNSIKILGRIKILTHRLCYVD-- 58
 Db 27 VKKADLNKNG-RFVALKRVKRVQTEEGMPL--STIREAVLRILETHEHPVAVNLFVCG 83
 QY 59 -ISKRHE-RELVVAHEGERSLEDLIRPKP---VSGSTVLCIAFEVIOGLQYMKHGV 113
 Db 84 TVSRDREKTLIVEHVDQDLTYL-DKVEPGVPTETIKMMQQLRGDLFHSRNV 142
 QY 114 HNALSPHNLIDKRIKILAKGLYHMTAHDVDFPIGYS-----YIAEVIAGCIF 167
 Db 143 HNDLKPNQLLVSSQIKIADEGLARL-----YSFQALTSVVVTLWYRAVEVLLQSSY 196
 QY 168 KTTDHMPKRPISPGSKSVWVSLGILLFEICVGRKLPFSLDISRLKFLTLDCVDTL 226
 Db 197 AI-----PY-----DLMSVGCIFAPMRPKRPLFGSSVDVGLKIL-----DVI 235
 QY 227 IVLAEEHGLDI-----IKELPEYIDLKRLKTHPSKRPPTDELM 268
 Db 236 GLPGEDMDPVALPQAFHKSAGPIEKFYVDIDELCKDLKLTLPNAKR----- 288
 QY 269 KIKVSVSPLYTPTFKASLHSSSLK---ADLTLPEDISQICNDIN 313
 Db 289 ----ISAVSALSHPY-----FDLERCKENLDSHP--SNTISELN 324

RESULT 9
 T52633
 serine/threonine-specific protein kinase (EC 2.7.1.-) AKIN1 [validated] - Arabidopsis
 N:Alternate names: SNF1 protein kinase omolog AKIN1
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 03-Nov-2000
 C:Accession: T52633
 R:Bhalerao, R.P.; Salchert, K.; Bairo, D.; Okresz, L.; Szabados, L.; Muranaka, T.; Machig
 Proc. Natl. Acad. Sci. U.S.A. 96, 5322-7, 1999
 A:Title: Regulatory interaction of PK1 WD protein with Arabidopsis SNF1-like protein ki
 A:Reference number: 225116; MUID:99238528
 A:Accession: T52633
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: mRNA
 A:Residues: 1-512 <BHA>
 A:Cross-references: EMBL:X99279; PIDN:CA67671.1
 A:Experimental source: cultivar Columbia
 C:Genetics:
 A:Gene: AKIN1
 C:Function:
 A:Description: EC 2.7.1.-; serine/threonine-specific protein kinase AKIN1 [validated, M
 complements SNF1 mutations in yeast

C:Superfamily: AMP-activated protein kinase; protein kinase homology
 C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase

Query Match 5.5%; Score 259; DB 2; Length 512;
 Best Local Similarity 21.9%; Prod. No. 1.3e-06;
 Matches 127; Conservative 83; Mismatches 193; Indels 176; Gaps 21;
 QY 35 SIKILGR-----FOILKTIHRLCYVDISKRKHELVVAHEGERSLE 79
 Db 47 AIKILNRKIKNMDEKVRREIKTLRPMRPHILROYEYLETSDIYVMEVYKSGELF 106
 QY 80 DLLEKRPVSSTVLCIAFEVIOGLQYMKHGVHRLSPHNLIDKRIKILAKPLDV 139
 Db 107 DYIEKGLDEDEKRNPFQVITISGVECHRMVYHRLKPPNLIDSKNIKIADEGLSN 166
 QY 140 MTAGDDVDFTIYGPSYIAPEVIAOGIPKTIIDHMSKRPISGKSVWSLGIILPEIAY 199
 Db 167 VMROGHLEIKTSGSPNVAAPVTSKILY-----ASPEVWWSGVVILVALDG 214
 QY 200 GRKLPSLIDISERKFLITLTKVNDTLIVLAEEHGLDIKELPEYIDLKLTTHPS 259
 Db 214 GLPFDENIPNIFKKI-----KGIYTLPSHLSSEARDLIPKMLIVPV 278
 QY 260 KRPPDELMKDVSVSPLYTPTFKASLHSSSLKQADLTLPEDISQICNDINNOYLAE 319
 Db 259 KRITPEIKCHRMVQTHLPRLANS-----PPDYEOAKKINE----- 296
 QY 320 RSIEEYVYLMCLAGDELEKLVNKEIIRSKPICLPNLFEEDESGGGRDRSLD-- 377
 Db 297 -----ETVGEVYN-----MGDRNOVLESL 316
 QY 378 -----DTVTLSLCQLNRKIDVCG--FAFVPLEDDQSN-----LPHS 414
 Db 317 RNRTQNDATVYVLL-LDNRKRVPSGVLESEFQETTSQSGSPMRTPGACSPVGHMTPAR 375
 QY 415 NSNNELSAATLPLIREKDEYOLN-----RIILFDRLKAVPYKKNQIMKEARVDI 467
 Db 376 VDHRGLGARSQVYV-----DKKMLGIGSHAPREIN-NVYAKL-DELVWCKK-----I 424
 QY 468 PPLKRGITWALLG-----VKGAIHAKYDA--LDKTPPL--PTDRQIPVYIPRCHQYDE 517
 Db 425 GHYNNKCHWVGGLDGGNTVWVNOJHFRDESSIIEDKAMTSPTVIAKFEILDYKAREEKY 484
 QY 518 ILSPEGHAKFRVYKAMVYSHRPLVWOGDLSLCAFL 556
 Db 485 LDIQIR-----VNGPQFLP--LD-LCAAFIL 506

RESULT 10
 T10449
 probable serine/threonine-specific protein kinase (EC 2.7.1.-) cucumber
 N:Alternate names: SNF1-related protein kinase
 C:Species: Cucumis sativus (cucumber)
 C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 20-Jun-2000
 C:Accession: T10449
 R:Gimpel, N.J.
 submitted to the EMBL Data Library, December 1996
 A:Reference number: Z17020
 A:Accession: T10449
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: mRNA
 A:Residues: 1-504 <GUM>
 A:Cross-references: EMBL:Y10036
 A:Experimental source: cv. Masterpiece; cotyledon
 C:Function:
 A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threo
 C:Superfamily: AMP-activated protein kinase; protein kinase homology
 C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
 F:6-260/Domain: protein kinase homology <KIN>
 Query Match 5.4%; Score 257; DB 2; Length 504;

best local similarity 22.48; prot. No. 1,66; db: 100; matches: 86; conservation: 94; mismatches: 129; indels: 114; gaps: 7;

QY 45 SIKLIRK FOLTKTTHPRQVYVDSKGRHRLVVAAGERSLE 79
 DB 45 AKILNRKIKNLMEERKREIKLRFMDPHILREYEVETPSDIYVVAEYKSGLE 94
 QY 80 DLLEKREKVSSTVLAFAVYGLQYNNKIGIVHRAISPINLLDKRGHKLAKPGYH 139
 DB 95 DYLVKRGIGDRAVNPQGLISVEYGRKNNVHRLKPNLLDSKGNKIAFGISN 154
 QY 140 MTAHDAVDFLTGYSTAPVLAQGTETTDHMSKKYLSGKSNWSLGLILPELV 199
 DB 155 LPRDHFKTSQSNVAAPVLSKRY AGHVDVWSGVLITALLG 201
 QY 200 GSKLFQSLDASRKELTLKVDITLVLAEEHGCLAEKEIDPEVYDILNKLTLEHS 259
 DB 202 GLTPEDENITNPKKI KGLTTPSHLSGAEHLPSMLVPRM 246
 QY 240 KRPTHELMKRVSEVSPLYTPTRKVASLSSSLRCADLTPLDLSQGLINDYLAE 319
 DB 247 KRPTHELRHWPQAHLPYLAVP PRDMOAKRIIDDL 287
 QY 420 RSTEEVYVLTAVGDEKELVNKEIDSKPTPTLNNLEPEDESGQGRSSILADPT 379
 DB 288 QEVVK MDRHOLIVE 302
 QY 480 TVTLSTVQLNRKIDVGEAFVPLED 406
 DB 403 SLNRKQNAIVAVYLLDN 422

RESULT 11

100/706
 Probable serine/threonine-specific protein kinase (EC 2.7.1.-) SNF1 - potato
 NEAtotide name: StbSNF1 protein
 C2Species: Solanum tuberosum (potato)
 C2date: 14 May 1999 #sequence_revision 14 May 1999 #text change 21-Jan-2000
 C2Accession: T07788
 Relatdss: 1.2 Rantala, V.
 submitted to the EMBL data library, January 1999
 A2refseq number: 216133
 A2Accession: T07788
 A2Status: preliminary; translated from cDNA/EMBL/GenBank
 A2Molecule type: mRNA
 A2Cross-reference: EMBL:084797; NID:q194915; P108:AA052224.1; P10:q194916
 A2Gene: SNF1
 A2Function:
 A2Description: catalyzes the formation of peptidyl serine phosphate or peptidyl threonate
 C2Superfamily: AMP-activated protein kinase; protein kinase homology
 C2Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
 E17.271/biomat: protein kinase homology - KIN.

Query Match 5.48; Score 256.5; DB 2: Length 512;
 best local similarity 21.98; prot. No. 1,86; db: 100;
 matches: 104; conservation: 71; mismatches: 166; indels: 141; gaps: 12;

QY 45 SIKLIRK FOLTKTTHPRQVYVDSKGRHRLVVAAGERSLE 79
 DB 46 AVKILNRKIKNLMEERKREIKLRFMDPHILREYEVETPSDIYVVAEYKSGLE 105
 QY 80 DLLEKREKVSSTVLAFAVYGLQYNNKIGIVHRAISPINLLDKRGHKLAKPGYH 139
 DB 106 DYLVKRGIGDRAVNPQGLISVEYGRKNNVHRLKPNLLDSKGNKIAFGISN 165
 QY 140 MTAHDAVDFLTGYSTAPVLAQGTETTDHMSKKYLSGKSNWSLGLILPELV 199
 DB 166 LPRDHFKTSQSNVAAPVLSKRY AGHVDVWSGVLITALLG 212
 QY 200 GSKLFQSLDASRKELTLKVDITLVLAEEHGCLAEKEIDPEVYDILNKLTLEHS 259

DB 213 GLTPEDENITNPKKI KGLTTPSHLSGAEHLPSMLVPRM 246
 QY 260 KRPTHELMKRVSEVSPLYTPTRKVASLSSSLRCADLTPLDLSQGLINDYLAE 319
 DB 258 KRPTHELRHWPQAHLPYLAVP PRDMOAKRIIDDL 287
 QY 420 RSTEEVYVLTAVGDEKELVNKEIDSKPTPTLNNLEPEDESGQGRSSILADPT 379
 DB 299 QEVVK MDRHOLIVE 302
 QY 480 TVTLSTVQLNRKIDVGEAFVPLED 406
 DB 414 SLNRKQNAIVAVYLLDN 422
 QY 440 NRILPRDLKAPVYKKNOLMEKRAVDIPLKRGILMAALGVSAIHR 489
 DB 355 NRINSNEPLDQWQRPGLMDQACARQPTER-KWA-LGIQSRHRR 401

RESULT 12

104/145
 serine/threonine protein kinase homolog - rice
 C2Species: Oryza sativa (rice)
 C2date: 24 Apr 1999 #sequence_revision 24-Apr-1999 #text change 21-Jan-2000
 C2Accession: T04145
 Relatdss: 1.3; 1.6; R.L.
 submitted to the EMBL data library, April 1996
 A2refseq number: 215249
 A2Accession: T04145
 A2Status: preliminary; translated from cDNA/EMBL/GenBank
 A2Molecule type: mRNA
 A2Cross-reference: EMBL:055768; NID:q1477683; P108:AA05457.1; P10:q1477684
 A2Gene: OsSNF1
 A2Function:
 A2Description: catalyzes the formation of peptidyl serine phosphate or peptidyl threonate
 C2Superfamily: AMP-activated protein kinase; protein kinase homology
 E17.270/biomat: protein kinase homology - KIN.

Query Match 5.48; Score 256.5; DB 2: Length 510;
 best local similarity 24.08; prot. No. 2,26; db: 100;
 matches: 92; conservation: 57; mismatches: 122; indels: 119; gaps: 10;

QY 45 SIKLIRK FOLTKTTHPRQVYVDSKGRHRLVVAAGERSLE 78
 DB 44 AKILNRKIKNLMEERKREIKLRFMDPHILREYEVETPSDIYVVAEYKSGLE 102
 QY 79 DLLEKREKVSSTVLAFAVYGLQYNNKIGIVHRAISPINLLDKRGHKLAKPGYH 137
 DB 103 DYLVKRGIGDRAVNPQGLISVEYGRKNNVHRLKPNLLDSKGNKIAFGISN 162
 QY 148 MTAHDAVDFLTGYSTAPVLAQGTETTDHMSKKYLSGKSNWSLGLILPELV 197
 DB 163 SNVNHKSHFKTSQSNVAAPVLSKRY AGHVDVWSGVLITALLG 209
 QY 198 GSKLFQSLDASRKELTLKVDITLVLAEEHGCLAEKEIDPEVYDILNKLTLEHS 257
 DB 210 LPRDHFKTSQSNVAAPVLSKRY AGHVDVWSGVLITALLG 264
 QY 258 KRPTHELMKRVSEVSPLYTPTRKVASLSSSLRCADLTPLDLSQGLINDYLAE 317
 DB 255 KRPTHELRHWPQAHLPYLAVP PRDMOAKRIIDDL 287
 QY 418 RSTEEVYVLTAVGDEKELVNKEIDSKPTPTLNNLEPEDESGQGRSSILADPT 377
 DB 298 QEVVK MDRHOLIVE 302
 QY 478 TVTLSTVQLNRKIDVGEAFVPLED 406
 DB 310 SLNRKQNAIVAVYLLDN 422

RESULT 13

JC1446

serine/threonine-specific protein kinase (EC 2.7.1.-) AK21 - Arabidopsis thaliana

N:Alternate names: protein kinase SNF1 homolog

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text_change 11-Jun-1999

C:Accession: JCI446; S58265; S66334

R:Klecken, L.; Thomas, M.; Bianchi, M.; Halford, N.G.; Kreis, M.

Gene 120, 249-254, 1992

A:Title: Structure and expression of a gene from Arabidopsis thaliana encoding a protein

A:Reference number: JCI446; MUID:93013041

A:Accession: JCI446

A:Molecule type: DNA

A:Residues: 1-512 <EB>

A:Cross-references: GB:M93023; NID:q166599; PIDN:AAA32736.1; PID:q166600

R:Thummler, F.; Kirchner, M.; Teuber, R.; Dittrich, P.

A:Submitted to the EMBL Data Library, May 1995

A:Description: Differential accumulation of the transcripts of 22 novel protein kinase g

A:Reference number: S58256

A:Accession: S58256

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 144-198 <TH>

A:Cross-references: EMBL:X86966; NID:q928909; PIDN:CAA60529.1; PID:q928910

R:Thummler, F.; Kirchner, M.; Teuber, R.; Dittich, P.

A:Plant Mol. Biol. 29, 551-555, 1995

A:Title: Differential accumulation of the transcripts of 22 novel protein kinase genes 1

A:Reference number: S66314; MUID:96123233

A:Accession: S66314

A:Molecule type: DNA

A:Residues: 144-198 <TH>

A:Cross-references: EMBL:X86966; NID:q928909; PIDN:CAA60529.1; PID:q928910

C:Comment: This enzyme plays an important role in a signal transduction cascade regulati

C:Genetics:

A:Gene: AK10; AK21

A:Introns: 64/1; 125/3; 186/3; 230/3; 292/3; 322/3; 350/3; 396/3; 475/3

C:Function:

A:Superfamily: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin

C:Keywords: ATP; magnesium; phosphotransferase; serine/threonine-specific protein kinase

F:17-271/Domain: protein kinase homology <KIN>

F:25-33/Region: protein kinase ATP-binding motif

F:148,67,142,144/Active site: Lys, Glu, Asp, Lys #status predicted

F:147,151/Binding site: magnesium (Asn, Asp) #status predicted

Query Match 5.3%; Score 252; DB 1; Length 512;

Best local similarity 22.0%; Pred. No. 36-06;

Matches 85; Conservative 59; Mismatches 129; Indels 114; Gaps 7;

QY 35 SLKILGR-----FQILKTTTTPRLCYVDISKGRHRLVVAEHCERSLR 79

DB 46 ALKILRRKIKNMEEKYRREIKILRLPHPHILKLYEVIETPTDYLMEVEVNSGELE 105

QY 80 DLIRKKRPVSGSVCTAFVYLOGLOYMKNKHGIVHRLSPHILLDRKHILAKRGILX 139

DB 106 DYVYEGKGLQDEBARNFPOOITSGVEYGRNMYVHRLKPEMLDLSKCNVAKIADQSLN 165

QY 140 MLAGGADVDFPIGYPSYLAPEVLAQGIFFKTTDMPKSKPLPSGKSDVWSLGIIPELCV 199

DB 166 IMDGHFILKTSQSPVYAPAEVLSCKLY-----ADPEVDVSGCVIILYALLIC 212

QY 200 GKLFPSLDLISERIKFLTLIDCVDTLLVLAEEHGLDIIKEIPETVIDLKLKCLTFHPS 259

DB 213 GTLPEDDENIPNLFRKI-----KGGIYITLPSHLSPGARDLIFRMIVVDDPM 257

QY 260 KRTPPELKKDKKVESEVPIYPTPKPASIFSSSLKGCALDLPEDISQAKOINNNYLA 319

DB 258 KRATTEILKQHWFOAHLPYLAAP-----PDDVQAKKIDEEIL-- 298

QY 320 RSTEEVYIMCLAGDLEKELVKEIIRSKPICTLPNLFEDGESFGGRHSSILDDT 379

DB 299 -----QGVIN-----MGDRNHLIF-- 313

QY 360 TVTSLQRLNRKLDVGEAFYPLIED 406

DB 314 -----SLRNKTNMGIVTYVILLDN 333

RESULT 14

A48144

protein kinase CDC5 (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae)

N:Alternate names: protein kinase PKX2; protein YM8270.03c; protein YMR001c

C:Species: Saccharomyces cerevisiae

C:Date: 30-Jun-1995 #sequence revision 30-Jun-1995 #text_change 24-Sep-1999

C:Accession: A48144; S53030; S27445

R:Kitada, K.; Johnson, A.L.; Johnston, L.H.; Sugino, A.

Mol. Cell. Biol. 13, 4445-4457, 1993

A:Title: A multicopy suppressor gene of the Saccharomyces cerevisiae G-1 cell cycle m

A:Reference number: A48144; MUID:93309479

A:Accession: A48144

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-705 <KIT>

A:Cross-references: EMBL:M84220; NID:q172186; PIDN:AAA02576.1; PID:q172187

R:Devlin, K.; Churcher, C.M.

A:Submitted to the EMBL Data Library, March 1995

A:Reference number: S53028

A:Accession: S53030

A:Molecule type: DNA

A:Residues: 1-705 <DEV>

A:Cross-references: EMBL:Z48613; NID:q728645; PIDN:CAA68516.1; PID:q728648; MIPS:YMR0

A:Experimental source: strain AB972

C:Genetics:

A:Gene: SGD; CDC5; PKX2

A:Cross-references: SGD:S0004603; MIPS:YMR001c

A:Map position: 14K

A:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom

C:Keywords: ATP; cell cycle control; phosphotransferase; protein kinase

F:80-337/Domain: protein kinase homology <KIN>

Query Match 5.3%; Score 252; DB 2; Length 705;

Best local similarity 22.3%; Pred. No. 4,4e-06;

Matches 144; Conservative 108; Mismatches 241; Indels 154; Gaps 28;

QY 37 KILGRFQILKTTTTPRLCYVDISKGRHRLVVAEHCER-SLRLKRRKPVSGSTYLC 95

DB 125 KLLSEIQIHKSMSPHIVQFIDCFE-DISNVYITLIEICPNGLMELKRRKVLTEPEVRF 184

QY 96 IAFVEILOGIYNNKHGIVHRLSPHILLDRKHILAKRGILYHMTAHGVDVDP1-QY 154

DB 184 FTTQCGAIKRYMSRRVIRHRLKICNIFPDSVYNLKICHPGIAAVIAAFSEKRYITICGP 243

QY 155 SYLAPEVLAQGIFFKTTDMPKSKPLPSGKSDVWSLGIIPELCVGRKLFPSLDIS--E 211

DB 244 NYLAPEVL--MCKHSGH-----SPFYVIMSLGYMAIALIGKPPQARVNTIYE 291

QY 212 KILFLLTLDCVDTLLVLAEEHGLDIIKEIPETVID--LNLKCLFPHRSKRPDP 267

DB 292 RIK-----CRDFSPHOKRPISDCKILITROIISLDPIFSPSLTEI 331

QY 268 MKDKVSEVSPYIYPTPKPASIFSSSLKGCALDLPEDISQAKOINNNYLA 327

DB 332 M-DYVYFRGT--PPSPSTVMSAPNPD--IPF----- 361

QY 328 IMCLAGDLEKELVKEIIRSKPICTLPNLFEDGESFGGRHSSILDDT 387

DB 362 -----EGLVNV-----FKDMKESILLFSSMSNKKIQ 389

QY 388 LNRLLKDVGEAFYPLLEDQSN--LPHSNNSNLSAAATLPILIRKDTIYQ--LNRI 442

DB 390 KRDIYTSI--KSSIDKLEFYHQNRPFLPHS-----LSPOGTRKQKRYEVVDTEAQRRLNDL 442

QY 444 LLEDELKAYP YKKNOIMKFAHYDLEPL MGLTLMALLAVEGALIAKAYDALDKPPPT 499
 DB 444 APEALTRGGGQAVILKRELATSTNTYKSELSIKLASHHILNIVIA EAQYKMGGL 500
 QY 500 PTLGR QLE VULTRCHDYDELSSPECHAKPKR VKKA WVSHP 540
 DB 501 EKSLDKRKIDMVKRWVYSNRKHSYQJSTEDIGVLENGCTYVKADAEETWYISYD 560
 QY 541 TGVWQGLISIAAPELYLNENNEALAYAGMSAFTRKYLYNPKNSHYL 594
 DB 541 DEEEM VASHYLSSEKPELSRHLVYVDFAKYKAMLSRYSTGDEEYHKOVEL 615
 QY 595 VFSQMLAFHDELSNHLNEIGFIPDL ALPFLTFMTFVPPHKL 639
 DB 616 PVTYVKPFVMEISAGTFCGFNF KDHKRMASIKGKLVYTSISHE 661

RESULT 15

AV7286

Probable serine/threonine protein kinase (EC 2.7.1.-) fork - mouse

Species: Mus musculus (house mouse)

Database: 01 Jan 1995 *sequence revision 01 Dec 1995 *text_change 10-Sep-1997

Accession: AV7286

ReleaseDate: 1995; Alberts, G.F.; 600; Y: Winkles, J.A.

1. Biol. Chem. 270, 10451-10457, 1995

2. Title: Identification by targeted differential display of an immediate early gene encoding a protein kinase homologue

Accession: AV7286; MIM:395247749

Accession: AV7286

Accession: AV7286

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Accession: AV7286

Accession: AV7286

Accession: AV7286

Accession: AV7286

QY 488 AKYDALDKOTPTPTDQLEVDLPCHQYDELLSSPEGH AKFRVILKAWVSH 539
 DB 492 NPSTKHPSSMKS VIKALDPOGLTLK YFASYMROHLMKGGDLSSVEAEVAP 545
 QY 540 POLVYWGGLISIAAPELYLNENNEALAYAGMSAFTRKYLYNPKNSHYL 595
 DB 546 PELLQWKTQ ALMLFSDGTQVQVNFYGDHKLILSQWEHLV 588
 QY 596 VFSQMLAFHDELSNHLNEIGFIPDL VYAL 624
 DB 589 TFVARNRSACTYLASHILKOLGCSHDLKORLRYAL 622

Search completed: August 12, 2002, 09:05:30
 Job time: 3722 sec

Query Match 5.4% Score 251.5; DB 2; Length 641;
 Best Local Similarity 22.4%; Prod. No. 4.1e-06;
 Matches 142; Unmatched 91; Mismatches 256; Indels 145; Gaps 27;

QY 45 SIKLILAPOLIKTTTHPLQYVDLSK KHKRLVNVANHE-----RSLE 79
 DB 90 AKKVLPSQVAKPHQREKILNLELDLQHHIVKFSNHFADNITYLEHLSRKSIA 149
 QY 80 DILLERKIVSTVLAIEVLYGLQYKNGKGLVHALSPNILLDKGHILAKKGLYH 139
 DB 150 ILWKAKHITLLEPVYVYLKQILSLIKYLHKGILLHRLKLNFEETIDMELKVCDEGLAA 209
 QY 140 MTAKHIDVDFI QYSLAYEV IAGGLFKTHMPKSKPLPSPKSWSLGILLPEL 197
 DB 210 KLEPEQORRKLTCGPNVADPEVLKQG BGFAMVMSLGVVYTL 254
 QY 198 CWGKKIPOSILSEKIKLTLQCVQDITLVIAEHEGLDIKELPEVTIDLANKGLTFH 257
 DB 255 LQTSPTFEADIKR TYRCL KQVHTLPASLSLAP QLLAAILKAS 299
 QY 258 VSKKTPHELMKKQVSEVSLATPEFKVSLPSSSLKADLTLEPDISLQCKDINNDYL 317
 DB 300 PDKRSTFQILHDDPTKQ YLPDRLGV SSGVTVPDLPDNPASLPAKATKSLP 353
 QY 318 AKRS LEEVYVLTIA QDLEKELVKKELIRSKPPTCTLPNLEPDESEFQ 368
 DB 304 GKKKKKKKNSHSDJNVSLAVVSGQAVASLLEFAVEELSP KOTLASSDCEEE 408
 QY 409 G LVAIVVSSALDAIKRQV AMHFAQDPAFL AGRHETL 446
 DB 429 LTRKTEYQINRLLLEPDLKAVYKKNQIMKFAVDPDLMGLTLMALLAVEGALH 487
 DB 442 VVSKWVYS NRK GPGVQLS SRKAVV LFNQDTHMALSNKRTVHY 491

FT	NON TERM	1	1	
NO	SEQUENCE	507 AA	56845 MW	24050PF14061CF982 CIRC64
	Query Match	53.5%	Score 2523.5	DB 4: Length 507;
	Host Local Similarity	92.3%	Ident. No. 3,76-199;	
	Matches 483	Conservative	Mismatches 22	Indels 1; Gaps 1;
QY	188	LENRLEKDVGEAFYPLLEDDDSNLPHSNNSNLSAAATPLPIREKDFEYQINRIILEDKR	447	
DB	1	LENRLEKDVGEAFYPLLEDDDSNLPHSNNSNLSAAATPLPIREKDFEYQINRIILEDKR	60	
QY	448	LLKAVYKKNOIWKRFARDYIPELMGTLMAALAGVCAHAKYDAIDKDTPIPTIQGLEV	507	
DB	61	LLKAVYKKNOIWKRFARDYIPELMGTLMAALAGVCAHAKYDAIDKDTPIPTIQGLEV	120	
QY	508	DIPKHOVDELLSPFGIAKFRVYLKAVVNSIPDLYVMQGLDSCFAPLYLTFNNEALAY	567	
DB	121	CYSSTSVBELLSPEGIKFRVYLKAVVNSIPDLYVMQGLDSCFAPLYLTFNNEALAY	180	
QY	568	ACMSAFIPKLYLNPFLKINSHTVDFEYVSNQIAFHPELPSNHLNIGFTDLYALPWF	627	
DB	181	ACMSAFIPKLYLNPFLKINSHTVDFEYVSNQIAFHPELPSNHLNIGFTDLYALPWF	240	
QY	628	LTMFHVFPELKLPELMQTLTANSPEPECTVALIQQLKDRILANCFENETLLESDLP	686	
DB	241	LTMFHVFPELKLPELMQTLTANSPEPECTVALIQQLKDRILANCFENETLLESDLP	300	
QY	687	ETIDEEVRESINLEFWTKSATYVQGHQAPTKPSSNSGCKSSAFYSAECVDPKPTDLS	746	
DB	301	ETIDEEVRESINLEFWTKSATYVQGHQAPTKPSSNSGCKSSAFYSAECVDPKPTDLS	360	
QY	747	RKSLINLEKRSVSPRIASDQLDLCETLVTSHEKTPSKRSKPKLLVYIRNSEDP1	806	
DB	361	RKSLINLEKRSVSPRIASDQLDLCETLVTSHEKTPSKRSKPKLLVYIRNSEDP1	420	
QY	807	RKHINSINIPSSAFTACGELTGTCTYAMQCNFGKGVIVGVHAKITAEFAALVPMK	866	
DB	421	RKHINSINIPSSAFTACGELTGTCTYAMQCNFGKGVIVGVHAKITAEFAALVPMK	480	
QY	867	YPRITLHGKINKIKPTGLTTPSQI	894	
DB	481	YPRITLHGKINKIKPTGLTTPSQI	507	
RESULT 3				
QY#488				
DB	QY#488	PRELIMINARY:	PRG:	840 AA.
AC	QY#488:			
DE	01 MAY 2000 (TTEH0401, 13, Cleared)			
DE	01 MAY 2000 (TTEH0401, 13, last sequence update)			
DE	01 JUN 2001 (TTEH0401, 17, last annotation update)			
DB	CG4041 protein.			
DB	CG4041.			
DB	Drosophila melanogaster (Fruit fly).			
DB	Eukaryota: Metazoa: Arthropoda: Tracheata: Hexapoda: Insecta:			
DB	Phylogeny: Neoptera: Endopterygota: Diptera: Brachycera: Muscocom:Pha:			
DB	Ephydroidea: Drosophilidae: Drosophila.			
DB	NCBI_taxid 7227:			
DB	111			
DB	SEQUENCE FROM N.A.			
DB	STRAIN: BEKLEFF:			
DB	MEDLINE 20196006, PubMed 10731132:			
DB	RA Adams M.D., Goldfiker S.B., Holt R.A., Evans C.A., Goryunov J.D.,			
DB	RA Amaratunga P.G., Schierer S.E., Li P.W., Hoskins R.A., Gallo R.P.,			
DB	RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,			
DB	RA Sutton G.G., Wortman J.R., Vardoli M.D., Zhang Q., Chen L.X.,			
DB	RA Burton R.C., Roberts Y.-H.C., Blazo J.R.G., Champo M., Pfeiffer A.D.,			
DB	RA Wan K.H., Boyle A., Baker E.G., Holt R.A., Nelson C.R., Miklos G.L.G.,			
DB	RA Abuli J.F., Abeyaratne A., An H.-J., Andrews-Piarnkooch C., Baldwin D.,			
DB	RA Ballew K.M., Bast A., Alexandare J., Hayraktaroglu I., Haseley E.M.,			
DB	RA Beeson K.T., Benos P.V., Bertani R.P., Bhandari D., Bolshakov S.,			
DB	RA Borokova D., Hotchan M.R., Bouck J., Brokstein P., Brothier P.,			

RA Butlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahle C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Domnes M., Dugan-Rocha S., Durov R.C., Dunn P.,
 RA Dudin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabriella A.F., Gary N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gottrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heitman J.J., Hernandez J.R., Honick J.,
 RA Hostin D., Houston K.A., Howland T.J., Mei M.-H., Ikegami C.,
 RA Jajali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira G.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Maitel B., McIntosh T.C., Meled M.P., Mcherson D.,
 RA Mekulov G., Mitsuhashi N.V., Murphy C., Morris J., Moshefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacib J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Schoeller F., Shen H.,
 RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svrtens R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RA "The genome sequence of *Drosophila melanogaster*."
 RA Science 287:2185-2195(2000).
 RA EMBL: A003432; AAF4595.1; -
 DR FlyBase: FBgn0029736; CG4041.
 DR InterPro: IPR000719; Euk_Pkinase.
 DR InterPro: IPR000195; RabGAP_TBC.
 DR InterPro: IPR001763; Rhodanese_domain.
 DR Pfam: PF00069; Pkinase; 2.
 DR Pfam: PF00566; TBC; 1.
 DR SMART: SM00450; RHOD; 1.
 DR SMART: SM00164; TBC; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 KW ATP-binding; Transferase.
 KW SEQUENCE 840 AA; 95572 MW; AOC56C1DE2BF8E1F CRC64;

Query Match 37.6%; Score 1775.5; DB 5; Length 840;
 Best Local Similarity 42.3%; Pred. No. 3,2e-137;
 Matches 388; Conservative 133; Mismatches 277; Indels 119; Gaps 13;

QY 5 KDAEKGATFFRASALPHVCCSGNGLPLTPNSIKILGNQILKTHPLRCGYVDISRGKH 64
 DB 8 RECRICAVTFPAKLPFGVCCSGNGLPLTPNSIALIGRAQKLEKDEHLCQYLDVIRGKH 67
 QY 65 ERLVVAHCEERSEDLREKRPVCSIVLCIAFEVLQGLQYMKHNGVHRAHLSPHNLL 124
 DB 68 ERTIVSEYELGLSDYAMKRPILAIAQILKIFYOVACGINVLSNHLVAMNVEKRIIL 127
 QY 125 DRKG-HIKIANFGVYHMTAGSDVDVDFPIGSPSYLAPEVIAQITKTTDHPMSKRPSPGP 183
 DB 128 SSDGQKVLKFNGLHMTKGAAYVFPFGNIRYMAPERLL-----GLGNV 173
 QY 184 KSDVSLDILIFELCVGSKILFUSIDISRLKFLLLDKVDVDTIVLAEEHSGCLDIKRLP 243
 DB 174 KSDVSLAIVVVELLLEIEMPRKLSNVVKRIIAFKCSNGLAEKIAREHCHERYVMD 233
 QY 244 ETVILILKCKLTFHPSKRPVDELKMDKRVSEV-----SPLYTFPTPASIFSSSL 294
 DB 214 QRLKOLLESCISVLPKRPRLKRLKELFHEVFEVLLDKKQKQPL-SFETHEPLPL--L 289
 QY 295 KCADLTLPEDISOLCKDINDYLAERSIEEYVYVWCLAGDLKELVYKKEITRSKPICT 354
 DB 290 RC-----PLSQIYHLMQJACGVQAELEKKEGJIRSEAPILG 325
 QY 355 LPNLFEEGSEFGGRSSSLDDTIVTLISCOLKRLKDKVGGEAFYVLLDDGSNLPHS 414
 DB 326 LPQIVRLSGASVCGRSQAQIMDKVVPFLKALKILQRLSGPAAVYFPLASPPPAHFA 385

QY 415 NSNNELSAATPLILTEKOTFYQANRIILFDRLLKAVPKKKQYKKEAVDIPPLMRGL 474
 DB 386 RELQE-----LPILIRKKDI EYGFQFVRLLFARILGQYPTAEQREAAVDPPLLRGP 439
 QY 475 TWAALLVEGAIHAKYATIDKPTDIPDRILEVQIPRCHQYDELSSPEGHAFRRYLKA 514
 DB 440 TMAALL--EYVPRNSYAKIDKFTSTIDRQILEVQIPRCHQYDELSSPKHKKRLRLKA 497
 QY 535 VVWSPDILVWQGLDSCAPPELYLNFNNEALVACMSAFIPKLYLPELKDINSVIOEYL 594
 DB 498 VWTAPQYVWQGLDSTLAPPELYLNFNNEALVAFISIFKPIPKYLOWPELKDINSVIRYL 567
 QY 595 TVFSQMAIAPDRPELSNHLNEIGFIPDIYALPWTITMTHTPPLKRIHMLDITLGNSSP 654
 DB 558 SKFSQIAFHPRPILAOHLASIPIDELFALPWTITMTHTPPLKRIHMLDITLGNSSV 617
 QY 655 PFCIGVALIQQLRDRLANGNECILLFSDLPEDIRGCVRESINLCPTPKSATYQHA 714
 DB 618 PLFGIALRLVRLRSTLTLSGFNECILLFSDLPIDVMDGCVLESOKMEATPKSTIRHQA 677
 QY 715 QPAPRSSDSSGGRSSADYFAECPPDPKTDLSRESIPLNDLKSEVSPRISAEDLIDCEL 774
 DB 678 LRLQP-----PQALDIGADVDELKHLQDFQCPRIKAKIVQFLD- 716
 QY 775 TVTGHFTPKSKTKSSKPKILVYIRNSPFIIRHISGFINIPSAFTAEGETGQPYT 834
 DB 717 -----NSPAELALIDLRSVFEGRVHVSINIPPAIVQALQRIEALQVP 762
 QY 835 AMLNFKQKVIIVIGHAKHAFPAHVMK-----YR-----RIGIL 873
 DB 763 QLEAGLNGKTIIVCCSNHGHVSFVGHPILQIKLICKLKSPIISQFSNPLVACGVQRTCL 822
 QY 874 DGGIN---KIKPTQILT 887
 DB 823 HKGFNVLSIEPNIILIS 839
 RESULT 4
 Q18386 PRELIMINARY; PRT: 826 AA.
 AC Q18386;
 DT 01-NOV-1996 (TEMBLrel. 01, Created)
 DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
 DE C33F10.2 PROTEIN.
 GN C33F10.2.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditroidea;
 OC Rhabditidae; Rhabditinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA None;
 RT "Genome sequence of the nematode *C. elegans*: a platform for
 RT investigating biology. The *C. elegans* Sequencing Consortium."
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Chaise S.;
 RT "The sequence of *C. elegans* cosmid C33F10."
 RL submitted (Feb-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Waterston R.;
 RT Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
 RL EMBL: 049830; AAK31474.1; -
 DR InterPro: IPR000719; Euk_Pkinase.
 DR InterPro: IPR000195; RabGAP_TBC.

Q9P251
ID Q9P251 PRELIMINARY: PRT; 870 AA.
AC Q9P251:
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE KIAA1477 PROTEIN (FRAGMENT).
GN KIAA1477.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid:9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-20277482; PubMed-10819331;
RA Nadeau T., Kikuno R., Ishikawa K., Hirosewa M., Ohara O.;
RT "Prediction of the coding sequences of unidentified human
RT genes-XVII: The complete sequences of 100 new cDNA clones from brain
RT which code for large proteins in vitro."
RL DNA Res. 7:143-150(2000).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: AB040910; BAA96001.1; -;
DR HSSP: P00518; PKK.
DR InterPro: IPR000719; Euk_Pkinase.
DR InterPro: IPR001772; KAI.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR000449; UBA.
DR Pfam: PF02149; KAI; 1.
DR Pfam: PF00069; pkinase; 1.
DR SMART: SM00627; UBA; 1.
DR SMART: SM00220; S_TKC; 1.
DR SMART: SM00165; UBA; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding: Serine/threonine-protein kinase; Transferase.
KW NON_TER
SQ SEQUENCE 870 AA: 95931 MW: 62E5FA858DB04509 CRC64;

Query Match 6.1%; Score 286.5; DB 4; Length 870;
Best Local Similarity 26.5%; Pred. No. 1.4e-14;
Matches 110; Conservative 58; Mismatches 140; Indels 117; Gaps 18;

QY 31 LTPNSI-KILRFQILKTIITPRICQYVDISKGRHELVVAEHCERLELDLREKPPVS 89
DB 208 LNPISLQKLFREVRIMKILNHNIGEVDP-----LVAGRMKEKRAKFR----- 254
QY 90 CSTVICIAFEVYLGQYMNKKGIVHRAISPINILLDRKGHIKIAKFGIYHMTAGDDVDF 149
DB 255 -----QIVSAVQYCHOKYIVHRDLKAENILLDGMNLIKIADEFGSENEFTVGKRLDT 305
QY 150 PIGPYSYLAPEVIAQGIKTTDHHPSKKPLPSGKSDVWSLGIILFELCYGKRIKLFOSLDI 209
DB 306 FCGSPYLAPELF-QG-KKYD-----GPEVWWSLGVILYTLVSSSLPFDGQNL 352
QY 210 SE-----RLKFLITLDCVDDTLVLAEBHGCLDIKELPEYIDLINLKCTFPPS 259
DB 353 KEIRERVIAGKRYRIPFWSIDCE-----NLKKLILVNP1 387
QY 260 KRPTDELIMKDK---VFSEVSPLYTPPTKPAFLSSSLRCADLILPEDIISOLCKDINDY 316
DB 388 KRGSLEQIMKDRMMNVGHEEEL-KPYTEPDPDENDTKR-IDIVYWGFA---RDEINDA 442
QY 317 IAFRSIEFVYVYLMCLAGDLEKELVNKEILSKRPICITLPNLFPEDESGGQ-----RDR 372
DB 443 L1NQRVDEVMATYILDG-----RKPP-----EPFGSGSLSSGNCQGRSR 481
QY 373 -SSLDPTTV-----TSLICQLNNRLKIDVGEAFYPLLEDDQSNLPHSNS 416
DB 482 PSSDLNNSITQSPAHILKYGRSISANQGRFSDHAGRPISPAV---SYTKRQVANS 534

RESULT 7

Q9POL2
ID Q9POL2 PRELIMINARY: PRT; 795 AA.
AC Q9POL2:
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MARK.
GN MARK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid:9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhou H.J., Huang X.W., Zhou Y., Hu S.L., Yuan J.G., Qiang B.Q.;
RT "Cloning and Isolating Human MARK."
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: AF154845; AAF72103.1; -;
DR HSSP: O63450; IAO6.
DR InterPro: IPR000719; Euk_Pkinase.
DR InterPro: IPR001772; KAI.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR InterPro: IPR000449; UBA.
DR Pfam: PF02149; KAI; 1.
DR Pfam: PF00069; pkinase; 1.
DR SMART: SM00627; UBA; 1.
DR SMART: SM00220; S_TKC; 1.
DR SMART: SM00165; UBA; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding: Serine/threonine-protein kinase; Transferase.
KW
SQ SEQUENCE 795 AA: 88986 MW: 89C9ABF265D679CB CRC64;

Query Match 6.0%; Score 284.5; DB 4; Length 795;
Best Local Similarity 26.0%; Pred. No. 1.6e-14;
Matches 108; Conservative 64; Mismatches 148; Indels 95; Gaps 16;

QY 31 LTPNSI-KILRFQILKTIITPRICQYVDISKGRHELVVAEHCERLELDLREKPPVS 89
DB 96 LNPISLQKLFREVRIMKILNHNIGEVDP-----LVAGRMKEKRAKFR----- 155
QY 90 CSTVICIAFEVYLGQYMNKKGIVHRAISPINILLDRKGHIKIAKFGIYHMTAGDDVDF 149
DB 156 EKEARAKFRQIVSAVQYCHOKYIVHRDLKAENILLDGMNLIKIADEFGSENEFTVGKRLDT 215
QY 150 PIGPYSYLAPEVIAQGIKTTDHHPSKKPLPSGKSDVWSLGIILFELCYGKRIKLFOSLDI 209
DB 216 FCGSPYLAPELF-QG-KKYD-----GPEVWWSLGVILYTLVSSSLPFDGQNL 262
QY 210 SE-----RLKFLITLDCVDDTLVLAEBHGCLDIKELPEYIDLINLKCTFPPS 259
DB 263 KEIRERVIAGKRYRIPFWSIDCE-----NLKKLILVNP1 297
QY 260 KRPTDELIMKDK---VFSEVSPLYTPPTKPAFLSSSLRCADLILPEDIISOLCKDINDY 316
DB 298 KRGSLEQIMKDRMMNVGHEEEL-KPYTEPDPDENDTKR-IDIVYWGFA---RDEINDA 452
QY 317 IAFRSIEFVYVYLMCLAGDLEKELVNKEILSKRPICITLPNLFPEDESGGQ-----RDR 372
DB 353 L1NQRVDEVMATYILDG-----RKPP-----EPFGSGSLSSGNCQGRSR 391
QY 373 -SSLDPTTV-----TSLICQLNNRLKIDVGEAFYPLLEDDQSNLPHSNS 416
DB 392 PSSDLNNSITQSPAHILKYGRSISANQGRFSDHAGRPISPAV---SYTKRQVANS 444

RESULT 8
040544

[illegible]

RESULT	9		
000678			
110	000678	PRELIMINARY:	PT: 793 AA.
AC	000678:		
DE	01-JUN-1997 (TREMUR1.04, Created)		
DE	01-JUN-1997 (TREMUR1.04, Last sequence update)		
DE	01-DEC-2001 (TREMUR1.19, Last annotation update)		
DE	SERINE/THREONINE KINASE.		
CN	MARK1		
CN	<i>Rattus norvegicus</i> (Rat).		
CN	Enkephalin; Melanin; Chondrin; Vertebral; Endocytosis;		
CR	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
CX	NCBI_TaxId=10110.		
KN	[1]		
KN	SEQUENCE OF 1-214 FROM N-ADP		
KN	STRAIN:STRATE-DAMLEY; TISSUE: BRAIN;		
KN	Medline:97262070; Pubmed:9106484;		
KA	Drewe G., Bineh A., Treuss U., Mandelkow E., Mandelkow E.;		
KA	"Markers of a Novel Family of Protein Kinases that Phosphorylate		
KT	Microtubule-associated Proteins and Tripartite Microtubule Disruption.";		
KL	Cell 89:297-308(1997).		

[illegible]

Db 216 FCGSPVYAPAELE-OG--KKYD-----GPEVDWMSLOVILYTLVSGSLPFDGQNL 262
 QY 210 SE-----KLKFLTLDCVDTLIVIAEEHGLIILKELPEVILDKLCTFPSP 259
 Db 263 KKLRRKRVLRGKRVVPFYSTDC-----NLKLLLVLP 297
 QY 260 KKPIDELMKDK--VFSEVSPLYPTPTKPSLFPSSLRCADLTPEDISQICNDY 316
 Db 298 KRGSLEQIMKDRMNVGHEEEL-KVSGSP-ELDLNDAKRIDIVTNGFA--RDEINDA 352
 QY 317 LAERIEEYVYLMCLAGDLEKELVKNELIRSKPICTLPNLFEDGESFGG--RDR 372
 Db 353 LVSOYKDEVMATYILG-----RKPP-----EFGEGESLSGNLCQRRS 391
 QY 373 -SSLDDTV-----TLSLCQLNRRLKDVGFAPYLL--EDDQSNLPHSNNN 418
 Db 392 PSSDINNSTLQSPALVKORISANQKORFSDHAGPSIPAVASTKPKQANVSESEKE 451
 QY 419 ELISAATLPLLRKDEYQYL 439
 Db 452 EW-----DKDIARLL 461

RESULT 10
 Q9ZNT4
 ID Q9ZNT4 PRELIMINARY: PRI: 508 AA.

AC Q9ZNT4: 01-MAY-1999 (TREMblrel. 10, created)
 DT 01-MAY-1999 (TREMblrel. 10, last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, last annotation update)
 DE OSK3.
 GN OSK3 OR OSK5.
 OS Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta;
 OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta;
 OC Spermatophyta: Magnoliophyta: Liliopsida: Poales: Poaceae;
 OC Eubacteriobacteriota: Oryzae: Oryza.
 NCBI_TaxID=4530;
 RX MEDLINE:99086251; PubMed:9670704;
 KA Takano M., Kajiya-Kanegae H., Funatsuki H., Kikuchi S.;
 RT "Rice has two distinct classes of protein kinase genes related to SNF1
 RT of Saccharomyces cerevisiae, which are differentially regulated in early
 RT seed development.";
 RL Mol. Gen. Genet. 260:388-394(1998).
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: D82038; BAA36297.1;
 DR EMBL: D82036; BAA36295.1;
 DR HSSP: Q63450; IA06.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR001772; KAT.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR InterPro: IPR000449; UBA.
 DR Pfam: PF02149; KAT.1.
 DR Pfam: PF00069; PKinase.1.
 DR Pfam: PF00627; UBA.1.
 DR PRINTS: PR00109; TYRKINASE.
 DR SMART: SM00220; S_TKc.1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP.1.
 DR PROSITE: PS0011; PROTEIN_KINASE_DOM.1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST.1.
 KM ATP-binding; Serine/threonine-protein kinase; Transferase.
 SO SEQUENCE 508 AA; 58250 MW; F935262080B39A59 CRC64;

Query Match 5.8%; Score 272; DB 10; Length 508;
 Best Local Similarity 23.9%; Pred. No. 9.6e-14;
 Matches 93; Conservative 57; Mismatches 121; Indels 118; Gaps 9;

QY 35 SIRIIGRFV-----IKTITPRICQYVDISRGKHERLVVAENGE-RSL 78
 Db 44 AIKILNRQMRNMMEKAKREIKILRLPIHPIITLVEVITPID-IYVMEVYCKFGL 102

QY 79 EDLIRKRPVSCSTVLCAIEEVLQGLQNMKHCIVHRLSPHNLDRKSHIKAKPGLY 138
 Db 103 FDIYVEKRLQDEDEARRLFOOIIISGEYCHRNMYVHDLKPNILLDSKNVNLADFGLS 162
 QY 139 HMTAHGDDVDFFIYPSYLAPEVIAQGIKFTQDHMPKSKPLPSQKSDVSLGILFELC 198
 Db 163 NVMDHGHILKISGSPVNAEVEVIGKLY-----ASPEVDWMSGVLLYAIL 209
 QY 199 VGRKLFQSLDSEKRLKILTLDCVDTLIVIAEEHGLDIIKELPEVILDKLCTFHP 258
 Db 210 CGLPFPDENIPNLFKRI-----KGLYTLPSHISALARDLIPMLVDP 254
 QY 259 SKRPTPELMKDKVSEVSPLYPTPTKPSLFPSSLRCADLTPEDISQICNDYLA 318
 Db 255 MKRTITREIRHOMFOURLPRYLAVP-----PPDIAQQAAMIDEVL- 256
 QY 319 ERSIEEYVYLMCLAGDLEKELVKNELIRSKPICTLPNLFEDGESFGGGRDSSLID 378
 Db 297 -----QDVVNIQYKGDH----- 308
 QY 379 TTVTLSCQ-LRNLKDVGFAPYLL 406
 Db 309 -----VCESLRNRLQNEATVAYVYLLDN 331

RESULT 11
 P87209
 ID P87209 PRELIMINARY: PRI: 602 AA.

AC P87209: 01-JUL-1997 (TREMblrel. 04, created)
 DT 01-JUL-1997 (TREMblrel. 04, last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, last annotation update)
 DE PUMATIVE KINASE.
 GN POG2.
 OS Kluyveromyces fragilis (Yeast).
 OC Eukaryota: Fungi: Ascomycota: Saccharomycotina: Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
 NCBI_TaxID=28985;
 RX SEQUENCE FROM N.A.
 RP STRAIN-2359/152;
 RA Goffredi P., Biondelli L., Iodi T., Perrezo L.;
 RT "Cloning and sequencing of POG2 a gene required for expression of
 RT glucose repressible genes in Kluyveromyces fragilis.";
 RL Genetics 29:316-326(1986).
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: X87975; CAA61235.1;
 DR HSSP: Q63450; IA06.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00069; PKinase.1.
 DR SMART: SM00220; S_TKc.1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP.1.
 DR PROSITE: PS0011; PROTEIN_KINASE_DOM.1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST.1.
 KM ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SO SEQUENCE 602 AA; 68618 MW; FC2558F4C83965EC CRC64;

Query Match 5.7%; Score 271; DB 3; Length 602;
 Best Local Similarity 23.3%; Pred. No. 1.5e-13;
 Matches 109; Conservative 84; Mismatches 189; Indels 86; Gaps 17;

QY 45 IKTITPRICQYVDISRGKHERLVVAENGE-RSL 104
 Db 87 LRLLRHPHILKIVYIKSGKDE-TIMVILYAGNELFDYIVQDKMPEDEARFFQOIIISAV 145
 QY 105 QYMKHGVHVALSHNLDRKSHIKAKPGLYHMTAHGDDVDFFIYPSYLAPEVIAQ 164
 Db 146 DYCHRKAKIVHDLKPNILLDRKSHIKAKPGLYHMTAHGDDVDFFIYPSYLAPEVIAQ 205
 QY 165 GIKFTDIMPCKPLPSQKSDVSLGILFELC-VGRKLFQSLDSEKRLKILTLDCVDT 224

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106 206 KLY ADEEVIWSSCVILYVM ----- ICRRLPPE --- DDE 235
07 229 TLEVLAE EGGDLDLKEPETVLDLNLKTLPIIDSKPPDELMKIVSEVSLY T 281
106 236 SLVPLFKRLSNVYTLNPLSLQASLLKRLLVNVNVTYVHELMQDEMKVLDLDDLY 295
07 262 PP -----TKVSLSSSSLCRQALTLPELDSQAK--DINNYLAKRS 321
106 296 DVESTHOFENSEKPKWGRSVPLFLDPLVQTLNLMYVLDLEVALSEDEHPSLNE 355
07 422 IEEVYVLMAGDLEKLVNKKELRSKPPDCTPLNPLEPESGQV-----GRORS 374
106 436 EDVAYQL KERNILIN DLRVNVQSDNDLPLSGSDPPEPESLMDPNSKNSH 409
07 475 LLDPTVTLSDVLQNLKQVGEAFVPLLEFQSNLHSSNNL SAAATPL 429
106 410 DREKRTDGRVGVYVHNSQJMDSTLALC FSSLDQTHRVNNVQGSQAARLSLIS 466
07 440 IREKRTVQLNKLTLPELLEKAVYKKNQIKKAKVDPPLMKDLYMA 477
106 467 VKRSKIPWH -----EGLRSRYPL DVMELVYALKNL GAWMA 503

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RESULT 12

09M726 PRELIMINARY: PRT: 514 AA.

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ID 01-OCT-2000 (TREMBLER, 15, Created)
AC 09M726
DT 01-OCT-2000 (TREMBLER, 15, Last sequence update)
DT 01-DEC-2001 (TREMBLER, 19, Last annotation update)
DE SNEI.
EN SNEI.
OS Lycopersicon esculentum (Tomato).
OC Eudicotyled. Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudots:
OC Asteridae: easterids 1: Solanales: Solanaceae: Solanum.
OC NCL TaxID 4081.
EN NCL
KA SEQUENCE FROM N.A.
KA Bradford K.L., Dohal P., Doolittle R., Nanopaki H., Alvarez V.,
KA "Yeast SNEI kinase homolog from tomato."
KA Submitted (Apr 1999) to the EMBL/Genbank/JDBI databases.
RT 1. SIMILARITY: BELONGS TO THE SNEI/FIR FAMILY OF PROTEIN KINASES.
DE EMBL: AF143743; AAF66639.1;
DE HSTB: Q63450; IAO6;
DE InterPro: IP000719; Euk PKinase.
DE InterPro: IP000772; KAT.
DE InterPro: IP0002260; Ser Thr PKinase.
DE InterPro: IP001245; Tyr PKinase.
DE InterPro: IP000449; DKA.
DE Pfam: Pf02149; KAT_1.
DE Pfam: PF00069; PKinase_1.
DE PRINTS: PF00109; TYRKINASE.
DE SMART: SM00202; S TKC_1.
DE SMART: SM00165; DHA_1.
DE PROSITE: PS00107; PROTEIN KINASE ATP_1.
DE PROSITE: PS0011; PROTEIN KINASE DM_1.
DE PROSITE: PS0108; PROTEIN KINASE ST_1.
KW ATP binding; Serine/threonine protein kinase; Transfester.
SQ
SEQUENCE 514 AA: 56825 MW: 98765211817PAC CRC64:

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Query Match 5.7% Score 270; DB 10; Length 514;
Post Local Similarity 22.9% Pred. No. 146 13;
Matches 9% Conservative 62; Mismatches 140; Indels 126; Gaps
07 45 SIKLIEH -----FOILKTLIPPLAGVVDLSKQKREKLVAVAEHESSE 79
106 46 AVKLILKKRLKRNQDEKVRREKTLGLDLMQDHLKLYEVETPSDLYVVEVKSGL 105
07 80 DILREKRVKSTVLGLAEVYLQTLQVNNKGLVHRLSPHNLIDKKCHLKLAKPGLYH 139

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DB 106 DYIWEKRLQDEAFARNFPGGLISGVFGRNNVYHRLDKNLILSSKNVXKLADEGLSN 165
07 140 MFAHDGVDFDIPYPSLAEVLAGGLFKTDHMPSSKRLPSGRKSVWSLGLILEFLV 199
DB 166 IMRCHNLEKTSQSPNVAPEVLSKRLY-----ADEEVIWSSCVILYALD 212
07 200 GRKLPSLIDISERKFLTLKVDPLVLAEHGLDILKEIPVVDLNLKTLPIIDSKPP 259
DB 213 GILPEFDENLHNLKRT-----KQILYLSHLSAARLDLPHMLLVDDM 257
07 260 KRLPDELMKIVSEVSLYTFPTKVASLSSSLKADLTPEPDSQAKDINNYLAE 319
DB 258 KRMTPPELRLHPVQALPPLAV-----PDTTGQAKKIDDEL 268
07 420 KSTEEVYLMAGDLEKLVNKKELRSKPPDCTPLNPLEPESGQVGRORSLLDPT 379
DB 299 -----QEVK -----MCPDRNNITE 313
07 480 TVTLISLQNLKQVGEAFVPLLEFQSNLHSSNNLSAAATPLIREKDEYQL 439
DB 314 -----SLRNVQNEETVAVYLLDN-----RHRVSTGYLGAF-----QESMEYGV 354
07 440 NRI 442
DB 355 NRI 357

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RESULT 13

096SW9 PRELIMINARY: PRT: 638 AA.

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ID 01-DEC-2001 (TREMBLER, 19, Created)
AC 096SW9
DT 01-DEC-2001 (TREMBLER, 19, Last sequence update)
DT 01-DEC-2001 (TREMBLER, 19, Last annotation update)
DE CUNA FL14587 FIS CLONE NTZM4001758. MURKATELY SIMILAR TO
DE EVATIVE SERINE/THREONINE PROTEIN KINASE EMK (EC 2.7.1.1).
OS Homo sapiens (human).
OC Eukaryota: Metazoa: Chordata: Vertebrata: Euteleostomi:
OC Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo.
OC NCL TaxID 9606;
EN NCL
KA SEQUENCE FROM N.A.
KA Isonagi T., Ota T., Hayashi K., Sugiyama T., Otsuki Y., Suzuki Y.,
KA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
KA Watanabe M., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
KA Takahashi M., Chiba Y., Ishida S., Murakami K., Iino Y., Takinuchi S.,
KA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
KA Yamamoto J., Wakamatsu A., Nakamura Y., Nagai T., Masuda Y.,
KA Niimura K., Iwayanagi T.
KA "NEED human cDNA sequencing project."
RT Submitted (May 2001) to the EMBL/Genbank/JDBI databases.
DE EMBL: AK027493; BAB5152.1;
SQ
SEQUENCE 638 AA: 71405 MW: 98279732570B0854 CRC64:

```

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Query Match 5.7% Score 268; DB 4; Length 638;
Post Local Similarity 28.0% Pred. No. 296 13;
Matches 97; Conservative 50; Mismatches 105; Indels 94; Gaps 15;
07 99 EVIQLQYNNKHCIVIRALSPHNLIDKKCHLKLAEGLYHMTAHDVDFPIGVSLA 158
DB 30 QIVSAVQYCHQKYVIRDLKAEMLILKDMNKLIAEFGPSNEFTVNNKLDITQGSPPYAA 89
07 159 PEVLAIAEKTIDHMSKRLPSGRKSVWSLGLILEFLVVDLNLKTLPIIDSKPP 211
DB 90 PELF-QS-KKYP-----GPEVYWSLGLVILYLSVSLSPVQVQNLKRLKRYLR 136
07 212 -----KLKELTLQGVDTLVLAEHGLDILKEIPVVDLNLKTLPIIDSKPP 268
DB 137 GKRYLPEYKSTDE-----NLLKLLVLMIRKQSLQDM 171
07 269 KQK-----VSEFVSLYTFEKPASTFSSSLQADLTLPEPDSQAKDINNYLAEKSTEEV 325

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DB 172 KQWMMVGEHEERL-KPTLEPDEFNDTKR-IDIMVTMGFA---KDEINDALINOKYDEV 226
 QY 326 YVIMCIAGCDLEKELVNKELIRSKPPICTLPNLFEDSEFCOG---RDR-SSLIDDT 380
 DB 227 MATYILIG-----KKRP-----FHEGGSLSGNCQNSRPSDLNST 265
 QY 381 V-----TSLCQLNRRLKDVGGFAFYPLLEDQSNLPHSN 416
 DB 266 LQSPALIKVORISANQKQRRFSDHAGPSIPPAV---SYTKRHOANS 309

RESULT 14

Q9ZRJ3 PRELIMINARY: PRT: 509 AA.
 AC Q9ZRJ3
 DT 01-MAY-1999 (TREMREL: 10, Created)
 DT 01-MAY-1999 (TREMREL: 10, Last sequence update)
 DT 01-DEC-2001 (TREMREL: 19, Last annotation update)
 DE OSK4.
 GN OSK4.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 KC MEDLINE:99086251; PubMed 9870704;
 RA Takano M., Kajiya-Kanegasa H., Funatsuki H., Kikuchi S.;
 *Rice has two distinct classes of protein kinase genes related to SNF1
 RT of Saccharomyces cerevisiae, which are differentially regulated in early
 seed development.*;
 RL Mol. Gen. Genet. 260:388-394(1998).
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DB EMBL: D82075; BAA56299.1;
 DR HSSP: Q63450; IAO6.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR001772; KAL.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR InterPro: IPR000449; URA.
 DR Pfam: PF00069; pkinase.1.
 DR Pfam: PF00627; URA.1.
 DR PRINTS: PR00109; TYRKINASE.
 DR SMART: SM00220; S_TKC.1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP.1.
 DR PROSITE: PS00011; PROTEIN_KINASE_DOM.1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST.1.
 KW ATP-binding; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 509 AA; 58471 MW; 6B82566D715A1B48 CRC64;

Query Match 5.6%; Score 264; DB 10; Length 509;
 Best local similarity 23.7%; Pred. No. 4, 4e-13;
 Matches 92; Conservative 57; Mismatches 122; Indels 118; Gaps 9;

QY 35 STILIGRFQ-----IKTTIHPRLCOYVDISRKHKRLVVAHCE-RSI 78
 DB 44 ALKILNRKQNRNMEKAKKELIKLRIPHPRIIRLEYEVIYTPD-IYVMVYCFGEI 102
 QY 79 EDILRRKPVSCSTVLICAFENILOGLYNNKRGIVRAHSPIHILDRKHILAKFGY 138
 DB 103 FQVIVKGRLOEIDARITVOILISVGYCHRNKVVIRIDIKPELLDLSKYNKLAFCGLS 162
 QY 139 HMTAGDNDVDFPIGYSYIAPVIAQGIKTTDHPMSKKPLPSGPKSVWSLGIILFELC 198
 DB 163 NVMHDEHFKTSCGSPNVAPEVILSGKY-----AGPEVDWSCGVILYALL 209
 QY 199 VGRKLFQSDISIRLKFILITLDCVDITLIVLAEEHGLDIIKRLPRTVIDILNKLCTFHP 258
 DB 210 CGTLFEDDENIPNIPFKKI-----KGIYTLPSHLASALARDLIPRMVLVDP 254

QY 259 SKRPTDELMDKQVSESVSPLYPTPTKPAISLSSSLRCADTLEPDISQLCKDINDYIA 318
 DB 255 MKRIIIRERHQMOWQIRLPHYLAAP-----PPPIAQAQKMLDEPIL- 296
 QY 319 ERSIFEVYLMCIAGDLEKELVNKELIRSKPPICTLPNLFEDSEFCOGSDRSSLLDD 378
 DB 297 -----QIVNVIAYEKDH----- 308
 QY 379 TTVTSLICQ-LRNRIKDVGGFAFYPLLED 406
 DB 309 -----VCESLRNRIQNEATVAYVILLDN 431

RESULT 15

Q15882 PRELIMINARY: PRT: 767 AA.
 AC Q15882
 DT 01-JAN-1998 (TREMREL: 05, Created)
 DT 01-JAN-1998 (TREMREL: 05, Last sequence update)
 DT 01-DEC-2001 (TREMREL: 19, Last annotation update)
 DE POLO-LIKE PROTEIN KINASE (FRAGMENT).
 GN PLK.
 OS Trypanosoma brucei.
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
 OX NCBI_TaxID=5691;
 RN [1]
 RP SEQUENCE FROM N.A.
 KC STRAIN-ST1B247;
 KC MEDLINE:98172736; PubMed 9511745;
 RA Graham T.M., Tall A., Hyde G.;
 *Characterisation of a polo-like protein kinase gene homologue from an
 RT evolutionary divergent eukaryote, Trypanosoma brucei.*;
 RL Gene 207:71-77(1998).
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DB EMBL: Y13468; CAA74301.1;
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR000959; POLO_box.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00069; pkinase.1.
 DR Pfam: PF00659; POLO_box.2.
 DR PRINTS: PR00109; TYRKINASE.
 DR SMART: SM00220; S_TKC.1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
 DR PROSITE: PS00011; PROTEIN_KINASE_DOM.1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST.1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 FT NON_TER 767
 SQ SEQUENCE 767 AA; 86823 MW; 8960E253F1F64D41 CRC64;

Query Match 5.5%; Score 260.5; DB 5; Length 767;
 Best local similarity 24.2%; Pred. No. 1, 6e-12;
 Matches 108; Conservative 71; Mismatches 140; Indels 127; Gaps 18;

QY 35 STILIGRFQIKTTIHPRLCOYVDISG-KHPRIV-----VVAEHG-ERSLE 79
 DB 68 ALKVDKSLQIKTLQKLSHSEISIRKAKIKHINPILRTFDDMNVIILPKSNOITLM 127
 QY 80 DLLRRKPVSCSTVLICAFENILOGLYNNKRGIVRAHSPIHILDRKHILAKFGY 138
 DB 128 ELTKRQRRSVETQYIALQISLAIQYMHQGVIRHDKIKGIMDAMNNVAKIGCFGLAA 187
 QY 139 HMTAGDNDVDFPIGYSYIAPVIAQGIKTTDHPMSKKPLPSGPKSVWSLGIILFELC 198
 DB 188 ELQYDGEKRRKTIQGPNTAPRIL-EGSBECHSY-----EVDVWSLGVILYLL 235
 QY 199 VGRKLFQSDISIRLKFILITLDCVDITLIVLAEEHGLDIIKRLPRTVIDILNKLCTFHP 250
 DB 236 VGRPPQTSVQVATYTRRIKQCHYRPPSHV-----VPSGSKELI 274
 QY 251 NKCLTFHPSKRPDPOLMKDKVSESVSPLYPTPTKPAISLSSSLRCADTLPEDISQ--- 307

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100 273 INSTLQSRFQDRTLLFHSHPPEKLPD PTTAPTTLPYSSRRKQJSDPQGIADGDL 331
007 10KH0NN0YLA FRS1EEVY1W1AGDLEKE1VNNK11ESKPP 351
100 442 P4P4QK3R10AAGKQTTQRRQ1Q5QKSVAVR QTS1RVSREV1Q-----P 380
007 452 ICT 1JN1LPEQESHPQUTROKSS1L1D1VTL5CQ1BNK1K1QVQCEAFY11L1D1QSN 410
100 481 1SFN1LPR -----TDR -----YH1K1S1P1AVASARF1G1G1K1M1C1NN 415
007 411 10JNSNN1L-----SAAATLP 427
100 416 NNNNNNN1NNA1NP1NSAAVSTP 439

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Search completed: August 12, 2002, 09:11:51
 Job Time: 488 sec

[illegible]

ID	AAH77995	standard; DNA: 3915 bp.		
XX	AAH77995:			
XX	13-NOV-2001	(first entry)		
XX				
DE	Nucleotide sequence of human protein kinase SGK382.			
XX				
KW	human; protein kinase; cancer; immune disease; cardiovascular disease;			
KW	brain disease; neuronal disease; Alzheimer's disease; chromosome 4;			
KW	Parkinson's disease; multiple sclerosis; metabolic disorder;			
KW	peripheral nervous system disease; amyotrophic lateral sclerosis;			
KW	infection; ocular disease; migraine; pain; sexual dysfunction;			
KW	mood disorder; attention disorder; cognition disorder; hypotension;			
KW	hypertension; psychotic disorder; dyskinesia; transplant rejection; SS.			
XX				
CS	Homo sapiens.			
XX				
PH	Key	Location/Qualifiers		
PH	CDS	1..3039		
ET		/*Id- d		
ET		/product: "protein kinase"		
XX				
PN	WO200166594-A2.			
XX				
PU	13-SEP-2001.			
XX				
PE	02-MAR-2001; 2001WO-US06838.			
XX				
PR	06-MAR-2000; 2000US-0187150.			
PR	29-MAR-2000; 2000US-0193404.			
PR	13-NOV-2000; 2000US-0247013.			
XX				
PA	(SUCE-) SUGEN INC.			
XX				
PI	Ploeman GD, Whyte D, Manning G, Sudarsanam S, Martinez R;			
XX				
DR	WPI: 2001-536777/59.			
XX	P-PSDR: AAC67396.			
PT	Nucleic acids capable of encoding human polypeptides having a kinase or			
PT	kinase-like activity, useful for diagnosing a disease selected from			
PT	cancers, cardiovascular disease and neuronal-associated diseases (e.g.			
PT	Alzheimer's disease) -			
XX				
PS	Example 1; Fig 1F-G; 201pp; English.			
XX				
CC	The present sequence encodes a human protein kinase. The gene is			
CC	located at chromosomal position 4q24. The kinase polypeptides are			
CC	useful for diagnosing a disease or disorder selected from cancers			
CC	(e.g. cancers of tissues and cancers of hematopoietic origin),			
CC	immune-related diseases and disorders, cardiovascular disease, brain			
CC	or neuronal-associated diseases (e.g. Alzheimer's disease, Parkinson's			
CC	disease, multiple sclerosis), metabolic disorders, peripheral nervous			
CC	system diseases, amyotrophic lateral sclerosis, viral infections,			
CC	infections caused by prions, infections caused by bacteria, infections			
CC	caused by fungi, ocular diseases, migraines, pain, sexual dysfunction,			
CC	mood disorders, attention disorders, cognition disorders, hypotension,			
CC	hypertension, psychiatric disorders, dyskinesias, and organ transplant			
CC	rejection. Kinase inhibitors are useful for treating diseases and			
CC	disorders described above.			
XX				
SO	Sequence 3915 BP: 1124 A; 847 C; 823 G; 1121 T; 0 other;			
Query Match 100.0%; Score 2682; DH 22; Length 3915;				
Best Local Similarity 100.0%; Prod. No. 0;				
Matches 2682; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
UY	1 atgttccctaaagaaacgtgaataaagaccttaccctctcttacctcgaacttccca 60			
	cc			
DB	358 agttctccctgaagaaacgtgaataaagaccttaccctctcttacctcgaacttccca 417			

[illegible][illegible]


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Db 2578 ccaaaacagatctgtcagagatctccatccatcaatgaagctgaagcagaatgata 2637
QY 2281 ccacgaatctccagacagagaccttgatgacttgctgagcagcagcagcagc 2340
Db 2638 cccacgaatctccagacagagaccttgatgacttgctgagcagcagcagcagc 2697
QY 2341 aaacacccacagacagacagcagcagcagcagcagcagcagcagcagcagc 2400
Db 2698 aaacacccacagacagacagcagcagcagcagcagcagcagcagcagcagc 2757
QY 2401 aatagtgagacatctatctgagcagcagcagcagcagcagcagcagcagc 2460
Db 2758 aatagtgagacatctatctgagcagcagcagcagcagcagcagcagcagc 2817
QY 2461 gaccttactgacagagagagagcagcagcagcagcagcagcagcagcagc 2520
Db 2818 gaccttactgacagagagagagcagcagcagcagcagcagcagcagcagc 2877
QY 2521 aaagagagagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2580
Db 2878 aaagagagagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2937
QY 2581 cacccttggagagagagagagcagcagcagcagcagcagcagcagcagc 2640
Db 2938 cacccttggagagagagagagcagcagcagcagcagcagcagcagcagc 2997
QY 2641 aaacacacagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2682
Db 2998 aaacacacagcagcagcagcagcagcagcagcagcagcagcagcagcagc 3039

RESULT 3
AAFS7407
ID AAF57407 standard; DNA; 2679 bp.
XX
AC AAF57407;
XX
DT 11-JUN-2001 (first entry)
XX
DE Human p100 protein encoding DNA.
XX
KW Rab; Rho; GTPase; pharmaceutical; cancer; anti-HIV; tuberculostatic;
KW protozoa; anti-diabetic; neotropic; neuroprotective; dermatological;
KW antipsoriatic; anti-inflammatory; antiallergic; antipyretic; cytostatic;
KW antibacterial; gynecological; antihypertensive; gene therapy; human;
KW p100; p95; p60; p45; p25; endocytic trafficking; GTPase effector; ds.
XX
OS Homo sapiens.
XX
FH Key 1 Location/Qualifiers
FT CDS 1..2679
FT /tag = a
FT /product "p100"
XX
IN W/200120022-A1.
XX
PI 22-MAR-2001.
XX
PF 18-SEP-2000; 2000MO-EP09140.
XX
PR 16-SEP-1999; 99EP-0118385.
XX
PA (PLAC ) MAX PLANCK GES FORBILDUNG WISSENSCHAFTEN.
PI Nielsen E, Christophoridis S, Murphy G, Zerial M, De Renzis S;
DR WPI: 2001-257888/26.
DR P-PSDB: AAB62179.
XX
PT Use of effectors of GTPase as target in a in vitro/vivo assay for
PT detecting substances for prophylaxis, treatment of cancer, cell
PT migration disorders, e.g. Alzheimer's, infectious diseases, diabetes,

```

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PT atherosclerosis
XX
NS Claim 10: Page 65-66; 76pp; English.
XX
CC The invention relates to the use of effectors/regulators for Rab and Rho
CC GTPases in in vitro or in vivo assays. The method is useful for detecting
CC substances useful as pharmaceutical agents for the prophylaxis or
CC treatment of cancer and other proliferative, invasive or cell migration
CC disorders such as endometriosis, atherosclerosis, inflammatory and
CC allergic diseases, infectious diseases, diabetes, Alzheimer's disease and
CC skin repair diseases such as psoriasis. The infectious diseases include
CC AIDS, tuberculosis, pseudotuberculosis, chlamydia, gastroenteritis, enteric
CC fever, malaria, lymphos, diseases caused by pathogens such as listeria,
CC Mycobacterium, Staphylococcus, Toxoplasma, Trypanosoma, Salmonella,
CC Legionella, Leishmania, Coxiella, Shigella, Yersinia, Neisseria, Vibrio,
CC Bartonella. The cancer includes benign tumor, malignant tumor, carcinoma,
CC leukemia, glioma or a neuroblastoma, in particular lung carcinoma,
CC osteosarcoma, lymphoma, breast, bile, intestine, kidney, ovary, stomach,
CC brain, prostate, liver and every tumor that invades other tissues and
CC organs distinct from its site of origin. The assay is highly sensitive
CC and advantageous in the selectivity of the targets. The present sequence
CC represents the DNA encoding a human p100 protein. A multiprotein complex
CC including p100, p95, p60, p45, p25 (sequences AAF57404-408) acts as a
CC GTPase effector/regulator and has the function of endocytic trafficking.
XX
SQ Sequence 2679 bp; 765 A; 576 C; 544 G; 794 T; 0 other;

Query Match 99.2%; Score 2659.6; DB 22; Length 2679;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2675; Conservative 0; Mismatches 4; Indels 3; Gaps 1;

QY 1 agcttccctgaagagagcagcagcagcagcagcagcagcagcagcagcagcagcagc 60
Db 1 agcttccctgaagagagcagcagcagcagcagcagcagcagcagcagcagcagcagc 60
QY 61 catgaatgttgagagagcagcagcagcagcagcagcagcagcagcagcagcagcagc 120
Db 61 catgaatgttgagagagcagcagcagcagcagcagcagcagcagcagcagcagcagc 120
QY 121 cgtcttcaaaccttcaaaccttcaaaccttcaaaccttcaaaccttcaaaccttcaaac 180
Db 121 cgtcttcaaaccttcaaaccttcaaaccttcaaaccttcaaaccttcaaaccttcaaac 180
QY 181 agggagagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 240
Db 181 agggagagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 240
QY 241 ttgcttcaaaccttcaaaccttcaaaccttcaaaccttcaaaccttcaaaccttcaaac 300
Db 241 ttgcttcaaaccttcaaaccttcaaaccttcaaaccttcaaaccttcaaaccttcaaac 300
QY 301 ctccaagccttcaaaccttcaaaccttcaaaccttcaaaccttcaaaccttcaaacctt 360
Db 301 ctccaagccttcaaaccttcaaaccttcaaaccttcaaaccttcaaaccttcaaacctt 360
QY 361 aatattccttgaagcagcagcagcagcagcagcagcagcagcagcagcagcagc 420
Db 361 aatattccttgaagcagcagcagcagcagcagcagcagcagcagcagcagcagc 420
QY 421 acagctcagatgagatgagatgagatgagatgagatgagatgagatgagatgagat 480
Db 421 acagctcagatgagatgagatgagatgagatgagatgagatgagatgagatgagat 480
QY 481 gtaattgcacagagagagagagagagagagagagagagagagagagagagagagag 540
Db 481 gtaattgcacagagagagagagagagagagagagagagagagagagagagagagag 540
QY 541 tctggcccaatcagatgagatgagatgagatgagatgagatgagatgagatgagat 600
Db 541 tctggcccaatcagatgagatgagatgagatgagatgagatgagatgagatgagat 600
QY 601 aaaaatatttcaagccttgaatatttcaagccttgaatatttcaagccttgaatattt 660

```


[illegible]

XX	immune system disorder; rheumatoid arthritis; inflammatory condition;
KM	organ transplant rejection; infection; hepatitis c; blood disorder;
KM	sickle cell anemia; hyperproliferative disorder; cancer's disease;
KM	neurodegenerative disorder; Alzheimer's disease; parkinson's disease;
KM	chromosomal abnormality; klinefelter syndrome; ischaemic heart disorder;
KM	cardiovascular; respiratory; wound healing; endocrine; Addison's disease;
KM	reproductive system; gastrointestinal; liver disorder; AIDS; SSI;
XX	acquired immune deficiency syndrome;
XX	Human sapiens -
XX	W020015473-A1.
XX	02-AUG-2001.
XX	17-JAN-2001; 2001WO-050141Z.
XX	31-JAN-2000; 200000S-0179065.
FR	04-FEB-2000; 200000S-0180628.
FR	04-FEB-2000; 200000S-0184664.
FR	02-MAR-2000; 200000S-0186450.
FR	16-MAR-2000; 200000S-0189874.
FR	17-MAR-2000; 200000S-0190076.
FR	18-APR-2000; 200000S-0198123.
FR	19-MAY-2000; 200000S-0205515.
FR	07-JUN-2000; 200000S-0209467.
FR	28-JUN-2000; 200000S-0214886.
FR	30-JUN-2000; 200000S-0215135.
FR	07-JUL-2000; 200000S-0216647.
FR	07-JUL-2000; 200000S-0216880.
FR	11-JUL-2000; 200000S-0217487.
FR	11-JUL-2000; 200000S-0217496.
FR	14-JUL-2000; 200000S-0218290.
FR	26-JUL-2000; 200000S-0220963.
FR	14-AUG-2000; 200000S-0224518.
FR	14-AUG-2000; 200000S-0224519.
FR	14-AUG-2000; 200000S-0225213.
FR	14-AUG-2000; 200000S-0225214.
FR	14-AUG-2000; 200000S-0225266.
FR	14-AUG-2000; 200000S-0225267.
FR	14-AUG-2000; 200000S-0225268.
FR	14-AUG-2000; 200000S-0225270.
FR	14-AUG-2000; 200000S-0225447.
FR	14-AUG-2000; 200000S-0225757.
FR	14-AUG-2000; 200000S-0225758.
FR	14-AUG-2000; 200000S-0225759.
FR	18-AUG-2000; 200000S-0226279.
FR	22-AUG-2000; 200000S-0226681.
FR	22-AUG-2000; 200000S-0226688.
FR	22-AUG-2000; 200000S-0227182.
FR	23-AUG-2000; 200000S-0227609.
FR	30-AUG-2000; 200000S-0228924.
FR	01-SEP-2000; 200000S-0229287.
FR	01-SEP-2000; 200000S-0229431.
FR	01-SEP-2000; 200000S-0229444.
FR	01-SEP-2000; 200000S-0229445.
FR	05-SEP-2000; 200000S-0229609.
FR	05-SEP-2000; 200000S-0229613.
FR	06-SEP-2000; 200000S-0230437.
FR	06-SEP-2000; 200000S-0230438.
FR	08-SEP-2000; 200000S-0231242.
FR	08-SEP-2000; 200000S-0231243.
FR	08-SEP-2000; 200000S-0231244.
FR	08-SEP-2000; 200000S-0231413.
FR	08-SEP-2000; 200000S-0231414.
FR	08-SEP-2000; 200000S-0232080.
FR	08-SEP-2000; 200000S-0232081.
FR	12-SEP-2000; 200000S-0231968.
FR	14-SEP-2000; 200000S-0232337.
FR	14-SEP-2000; 200000S-0232398.
FR	14-SEP-2000; 200000S-0232399.
FR	14-SEP-2000; 200000S-0232400.

[illegible]

PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251864.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251949.
PR 08-DEC-2000; 2000US-0251949.
PR 11-DEC-2000; 2000US-0254047.
PR 05-JAN-2001; 2001US-0254678.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PA Rosen CA, Barash SC, Rubin SM;
XX P1
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CC The invention relates to novel isolated polypeptides (I), and
CC polynucleotides (II), (I) and (II) and the antibody to (I) are useful for
CC diagnosing, preventing and treating diseases including immune system
CC disorders (e.g. congenital and acquired immunodeficiencies, autoimmune
CC disorders (e.g. rheumatoid arthritis), inflammatory conditions, organ
CC transplant rejections and graft versus host disease, infectious disease
CC (e.g. hepatitis C), bleeding disorders, haematological abnormalities and
CC other blood-related disorders (sickle cell anaemia), myeloproliferative
CC disorders, primary haematopoietic disorders, hyperproliferative
CC disorders (e.g. Gaucher's disease and cancer), neurodegenerative
CC disorders (e.g. Alzheimer's disease, Parkinson's disease), chromosomal
CC abnormalities (Down syndrome), ischaemic injury (e.g. stroke), renal
CC disorders (e.g. glomerulonephritis), cardiovascular disorders
CC (e.g. arrhythmia), respiratory disorders, dermatological disorders, in
CC wound healing, epithelial cell proliferation, endocrine disorders (e.g.
CC Addison's disease), reproductive system disorders, gastrointestinal
CC disorder (inflammatory disorders), liver disorders (cirrhosis),
CC as stimulators of B-cell responsiveness to pathogens, activators of
CC T-cells, to induce higher affinity antibodies, and as a means to induce
CC tumour proliferation in pathologies e.g. acquired immune deficiency
CC syndrome (AIDS). AAS26765-AAS2785) represent novel signal transduction
CC pathway protein coding sequences and their partners of the invention.

Query Match	73.18	Score 1961.4	IR 22	Length 2484
Best Local Similarity	99.68	Prod. No. 0		
Matches 1970: Conservative	4	Mismatches	2	Indels 1
				Gaps 1

QY	707	tgacatcataaagaagctctcgaacgtatgaatcttgaataaagcttacct	746
Pb	1	tggacattataaagaagctcttcgaacgtatgtaagcttttgaataagcttacct	60
QY	767	tccatccctctaaagaagcaccacccagatgaatlaataaagacaaagattcattgaag	826
Pb	61	tccatccctctaaagaagcaccacccagatgaatlaataaagaacaaagattcattgaag	120
QY	827	tataaccttatatacccccctttaccacaacctccagctctgatttcatctctcgaat	886
Pb	121	tataacctttatatacccccctttaccacaacctccagctctgatttcatctctcgaat	180
QY	887	gtacctgaatttaacrtctgcctcgaaagatcattcagctgattatgtataaagatataaataatgatt	946
Pb	181	gtacctgaatttaacrtctgcctcgaaagatcattcagctgattatgtataaagatataaataatgatt	240
QY	947	aacctgcaagaagaagctatttgaagaagatgatataccttgaatttgaagtcgaagaatgaat	1006
Pb	241	aacctgcaagaagaagctatttgaagaagatgatataccttgaatttgaagtcgaagaatgaat	300
QY	1007	tggagaaagaagctcttccaaagaagaatcatttgatcccaaacacctatctctgaacctc	1066
Pb	301	tggagaaagaagctcttccaaagaagaatcatttgatcccaaacacctatctctgaacctc	360

[illegible][illegible]

P1 Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J:
 P1 Zhao YA, Zhou P, Goodrich R, Ormanac RT:

XX WPT: 2001-442253/47.

XX P-PSDB: AAM40781.

P1 Novel nucleic acids and polypeptides, useful for treating disorders
 P1 such as central nervous system injuries -

XX Claim 1: SEQ ID NO 3926; 10078bp; English.

XX The invention relates to human nucleic acids (AA157798-AA161369) and
 CC the encoded polypeptides (AAM38642-AAM42213) with neurotropic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: immune system suppression,
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukemias and
 CC C.N.S disorders.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.

XX Sequence 1452 BP; 415 A; 287 C; 294 G; 456 T; 0 other;

Query Match 49.4%; Score 1325.8; DB 22; Length 1452;

Best Local Similarity 99.28; Pred No 0;

Matches 1374; Conservative 0; Mismatches 7; Indels 4; Gaps 4;

QY 596 tggaaagaaatattatcagagcttgaatattctgaaagaaatatttgcctact 655
 Db 1 taqgaagaaatattcagagcttgaatattctgaaagaaatatttgcctact 60
 QY 656 tgaattgttgaatgaatcttcaatgcttctgctgaagacatgcttcttgaagacta 715
 Db 61 tgaattgttgaatgaatcttcaatgcttctgctgaagacatgcttcttgaagacta 120
 QY 716 taagagagcttctgaagctgataagcttcttgaagagagcttcttgaagacta 775
 Db 121 taagagagcttctgaagctgataagcttcttgaagagagcttcttgaagacta 180
 QY 776 cttaag 835
 Db 181 cttaag 240
 QY 836 tatatacccccttaccagagctgagagcttcttcaatcttcttgaagagagagag 895
 Db 241 tatatacccccttaccagagctgagagcttcttcaatcttcttgaagagagagag 300
 QY 896 taactctgctgaagatataatcaatgcttgaagagagagagagagagagagagag 955
 Db 301 taactctgctgaagatataatcaatgcttgaagagagagagagagagagagagag 360
 QY 956 aaagatctatgaag 1015
 Db 361 aaagatctatgaag 420
 QY 1016 agcttctgag 1075
 Db 421 agcttctgag 480
 QY 1076 tcttgaag 1135
 Db 481 tcttgaag 540
 QY 1136 ctacatgacatctctatagcagagagagagagagagagagagagagagagagagag 1195

Db 541 ccaatgag 600
 QY 1196 catttaccatctacattgaagagagagagagagagagagagagagagagagagagag 1254
 Db 601 catttaccatctacattgaagagagagagagagagagagagagagagagagagagag 660
 QY 1254 tgaattgttgaatgaatcttcaatgcttctgctgaagacatgcttcttgaagacta 1313
 Db 661 tgaattgttgaatgaatcttcaatgcttctgctgaagacatgcttcttgaagacta 720
 QY 1314 actaaatgaatattcttctgagagagagagagagagagagagagagagagagagagag 1374
 Db 721 actaaatgaatattcttctgagagagagagagagagagagagagagagagagagagag 780
 QY 1374 aatctggaag 1433
 Db 781 aatctggaag 840
 QY 1434 tcttctgag 1493
 Db 841 tcttctgag 900
 QY 1494 aatctgaag 1553
 Db 901 aatctgaag 960
 QY 1554 gttatcatctctgag 1613
 Db 961 gttatcatctctgag 1020
 QY 1614 tcatctgaatcttctgag 1673
 Db 1021 tcatctgaatcttctgag 1080
 QY 1674 aaacttcaataaag 1733
 Db 1081 aaacttcaataaag 1140
 QY 1734 gtaatacttcttcaataaag 1793
 Db 1141 gtaatacttcttcaataaag 1200
 QY 1794 tgaatgag 1854
 Db 1201 tgaatgag 1260
 QY 1854 tccagatctctgag 1914
 Db 1261 tccagatctctgag 1320
 QY 1914 caaatcttccag 1971
 Db 1321 caaatcttccag 1480
 QY 1972 attgg 1976
 Db 1381 attgg 1385

RESULT 7
 AA196718
 ID AA196718 standard; cDNA; 754 BP.
 XX
 AC AA196718;
 XX
 DT 13-NOV-2001 (first entry)
 XX
 DE Human neuroblastoma expressed polynucleotide SEQ ID NO 2793.
 XX
 KW Human; neuroblastoma; malignancy; cancer; tumour marker; N-myc; TrkA; ss.
 XX
 OS Homo sapiens.
 XX

XX 04-FEB-2000: 2000US-0180412.
 PR 26-MAY-2000: 2000US-0207456.
 PR 30-JUN-2000: 2000US-060408.
 PR 03-AUG-2000: 2000US-063246.
 PR 21-SEP-2000: 2000US-0244687.
 PR 27-SEP-2000: 2000US-0236359.
 PR 04-OCT-2000: 2000US-0024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR:
 PT WPI: 2001-48897/53.
 DR
 XX
 PT Human genome-derived single exon nucleic acid probes useful for
 PI analyzing gene expression in human placenta.
 XX
 PS Claim 25: SEQ ID NO 12104; 654bp; English.
 XX
 CC The present invention relates to single exon nucleic acid probes (SENP).
 CC The present sequence is one such probe. The probes are useful for
 CC producing a microarray for predicting, measuring and displaying gene
 CC expression in samples derived from human placenta. The probes are useful
 CC for antenatal diagnosis of human genetic disorders.
 XX
 SU Sequence 589 BP: 215 A; 91 C; 100 G; 183 T; 0 other;

Query Match 6.7%; Score 178.6; DB 22; Length 589;
 Best Local Similarity 97.8%; Pred. No. 2,50-41;
 Matches 181; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 2056 cccgaattcagcattgaacgtctatgacgaacatcctatcctcttctgacatcct 2115
 DB 401 ctggaattcagcattgaacgtctatgacgaacatcctatcctcttctgacatcct 342
 QY 2116 aaaaagttcagcattgaacgtctatgacgaacatcctatcctcttctgacatcct 2175
 DB 341 aaaaagttcagcattgaacgtctatgacgaacatcctatcctcttctgacatcct 282
 QY 2176 ggcgaattcagcattgaacgtctatgacgaacatcctatcctcttctgacatcct 2235
 DB 281 ggcgaattcagcattgaacgtctatgacgaacatcctatcctcttctgacatcct 222
 QY 2236 tccag 2240
 DB 221 gtafg 217

RESULT 12
 ID AAI56397 standard: DNA: 177 BP.
 XX
 AC AAI56397;
 XX
 DE 17-OCT-2001 (first entry)
 XX
 DE Probe #25083 used to measure gene expression in human placenta sample.
 XX
 KW Probe: microarray; human; placenta; antenatal diagnosis;
 KW genetic disorder; ss.
 XX
 OS Homo sapiens.
 XX
 PN W0200157272-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001: 2001WO-0500663.
 XX
 PR 04-FEB-2000: 2000US-0180412.
 PR 26-MAY-2000: 2000US-0207456.

PR 30-JUN-2000: 2000US-0608408.
 PR 03-AUG-2000: 2000US-063246.
 PR 21-SEP-2000: 2000US-0244687.
 PR 27-SEP-2000: 2000US-0236359.
 PR 04-OCT-2000: 2000US-0024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR:
 PT WPI: 2001-48897/53.
 DR
 XX
 PT Human genome-derived single exon nucleic acid probes useful for
 PI analyzing gene expression in human placenta.
 XX
 PS Claim 25: SEQ ID NO 25083; 654bp; English.
 XX
 CC The present invention relates to single exon nucleic acid probes (SENP).
 CC The present sequence is one such probe. The probes are useful for
 CC producing a microarray for predicting, measuring and displaying gene
 CC expression in samples derived from human placenta. The probes are useful
 CC for antenatal diagnosis of human genetic disorders.
 XX
 SU Sequence 177 BP: 47 A; 38 C; 43 G; 49 T; 0 other;

Query Match 6.6%; Score 177; DB 22; Length 177;
 Best Local Similarity 100.0%; Pred. No. 3,80-41;
 Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2059 aaaaattcagcattgaacgtctatgacgaacatcctatcctcttctgacatcct 2118
 DB 177 gaaattcagcattgaacgtctatgacgaacatcctatcctcttctgacatcct 118
 QY 2119 aatcctcagcattgaacgtctatgacgaacatcctatcctcttctgacatcct 2178
 DB 117 agtctcagcattgaacgtctatgacgaacatcctatcctcttctgacatcct 58
 QY 2179 aaaaattcagcattgaacgtctatgacgaacatcctatcctcttctgacatcct 2235
 DB 57 aaaaattcagcattgaacgtctatgacgaacatcctatcctcttctgacatcct 1

RESULT 13
 ID AB107098 standard: cDNA: 5028 BP.
 XX
 AC AB107098;
 XX
 DE 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 15776.
 XX
 KW Drosophila; developmental biology; cell signaling; insect; ider;
 KW pharmaceutical; gene; ss.
 XX
 OS Drosophila melanogaster.
 XX
 PN W0200171042-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 23-MAR-2001: 2001WO-0509231.
 XX
 PR 23-MAR-2000: 2000US-191647P.
 PR 11-JUL-2000: 2000US-0614150.
 XX
 PA (PEKE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li TWD, Myers EW:
 XX
 DR WPI: 2001-656860/75.
 DR P-PSDB: ABB62945.

16	08	N-V	200003	0.246474.
17	08	N-V	200002	0.246475.
18	08	N-V	200001	0.246476.
19	08	N-V	200000	0.246477.
20	08	N-V	200000	0.246478.
21	08	N-V	200000	0.246479.
22	08	N-V	200000	0.246480.
23	08	N-V	200000	0.246481.
24	08	N-V	200000	0.246482.
25	08	N-V	200000	0.246483.
26	08	N-V	200000	0.246484.
27	08	N-V	200000	0.246485.
28	08	N-V	200000	0.246486.
29	08	N-V	200000	0.246487.
30	08	N-V	200000	0.246488.
31	08	N-V	200000	0.246489.
32	08	N-V	200000	0.246490.
33	08	N-V	200000	0.246491.
34	08	N-V	200000	0.246492.
35	08	N-V	200000	0.246493.
36	08	N-V	200000	0.246494.
37	08	N-V	200000	0.246495.
38	08	N-V	200000	0.246496.
39	08	N-V	200000	0.246497.
40	08	N-V	200000	0.246498.
41	08	N-V	200000	0.246499.
42	08	N-V	200000	0.246500.
43	08	N-V	200000	0.246501.
44	08	N-V	200000	0.246502.
45	08	N-V	200000	0.246503.
46	08	N-V	200000	0.246504.
47	08	N-V	200000	0.246505.
48	08	N-V	200000	0.246506.
49	08	N-V	200000	0.246507.
50	08	N-V	200000	0.246508.
51	08	N-V	200000	0.246509.
52	08	N-V	200000	0.246510.
53	08	N-V	200000	0.246511.
54	08	N-V	200000	0.246512.
55	08	N-V	200000	0.246513.
56	08	N-V	200000	0.246514.
57	08	N-V	200000	0.246515.
58	08	N-V	200000	0.246516.
59	08	N-V	200000	0.246517.
60	08	N-V	200000	0.246518.
61	08	N-V	200000	0.246519.
62	08	N-V	200000	0.246520.
63	08	N-V	200000	0.246521.
64	08	N-V	200000	0.246522.
65	08	N-V	200000	0.246523.
66	08	N-V	200000	0.246524.
67	08	N-V	200000	0.246525.
68	08	N-V	200000	0.246526.
69	08	N-V	200000	0.246527.
70	08	N-V	200000	0.246528.
71	08	N-V	200000	0.246529.
72	08	N-V	200000	0.246530.
73	08	N-V	200000	0.246531.
74	08	N-V	200000	0.246532.
75	08	N-V	200000	0.246533.
76	08	N-V	200000	0.246534.
77	08	N-V	200000	0.246535.
78	08	N-V	200000	0.246536.
79	08	N-V	200000	0.246537.
80	08	N-V	200000	0.246538.
81	08	N-V	200000	0.246539.
82	08	N-V	200000	0.246540.
83	08	N-V	200000	0.246541.
84	08	N-V	200000	0.246542.
85	08	N-V	200000	0.246543.
86	08	N-V	200000	0.246544.
87	08	N-V	200000	0.246545.
88	08	N-V	200000	0.246546.
89	08	N-V	200000	0.246547.
90	08	N-V	200000	0.246548.
91	08	N-V	200000	0.246549.
92	08	N-V	200000	0.246550.
93	08	N-V	200000	0.246551.
94	08	N-V	200000	0.246552.
95	08	N-V	200000	0.246553.
96	08	N-V	200000	0.246554.
97	08	N-V	200000	0.246555.
98	08	N-V	200000	0.246556.
99	08	N-V		

multiple sclerosis, rheumatoid arthritis and ulcerative colitis;
(c) cardiovascular disorders such as myocardial ischaemias; (d) wound
healing; (e) neurological diseases e.g. cerebral anaemia and epilepsy;
(f) and (f) infectious diseases such as viral, bacterial, fungal and
parasitic infections.

Note: The sequence data for this patent did not form part of the
patent specification, but was obtained in electronic format directly
from WHO at http://who.int/pub/publicated_pat_sequences.

Query Match 2.58; Score 67.2; DB 22; Length 1056.

Matches: 102; Conservative: 0; Mismatches: 58; Indels: 0; Gaps: 0.

[illegible][illegible]

γ

$$\{1, 2, \dots, n\} \rightarrow \{1, 2, \dots, n\} \text{ is a permutation of } \{1, 2, \dots, n\} \text{ if and only if it is a bijection.}$$
[illegible]

121 1. 2. 3. 4. 5. 6. 7. 8. 9. 10. 11. 12. 13. 14. 15. 16. 17. 18. 19. 20. 21. 22. 23. 24. 25. 26. 27. 28. 29. 30. 31. 32. 33. 34. 35. 36. 37. 38. 39. 40. 41. 42. 43. 44. 45. 46. 47. 48. 49. 50. 51. 52. 53. 54. 55. 56. 57. 58. 59. 60. 61. 62. 63. 64. 65. 66. 67. 68. 69. 70. 71. 72. 73. 74. 75. 76. 77. 78. 79. 80. 81. 82. 83. 84. 85. 86. 87. 88. 89. 90. 91. 92. 93. 94. 95. 96. 97. 98. 99. 100. 101. 102. 103. 104. 105. 106. 107. 108. 109. 110. 111. 112. 113. 114. 115. 116. 117. 118. 119. 120. 121. 122. 123. 124. 125. 126. 127. 128. 129. 130. 131. 132. 133. 134. 135. 136. 137. 138. 139. 140. 141. 142. 143. 144. 145. 146. 147. 148. 149. 150. 151. 152. 153. 154. 155. 156. 157. 158. 159. 160. 161. 162. 163. 164. 165. 166. 167. 168. 169. 170. 171. 172. 173. 174. 175. 176. 177. 178. 179. 180. 181. 182. 183. 184. 185. 186. 187. 188. 189. 190. 191. 192. 193. 194. 195. 196. 197. 198. 199. 200. 201. 202. 203. 204. 205. 206. 207. 208. 209. 210. 211. 212. 213. 214. 215. 216. 217. 218. 219. 220. 221. 222. 223. 224. 225. 226. 227. 228. 229. 230. 231. 232. 233. 234. 235. 236. 237. 238. 239. 240. 241. 242. 243. 244. 245. 246. 247. 248. 249. 250. 251. 252. 253. 254. 255. 256. 257. 258. 259. 260. 261. 262. 263. 264. 265. 266. 267. 268. 269. 270. 271. 272. 273. 274. 275. 276. 277. 278. 279. 280. 281. 282. 283. 284. 285. 286. 287. 288. 289. 290. 291. 292. 293. 294. 295. 296. 297. 298. 299. 300. 301. 302. 303. 304. 305. 306. 307. 308. 309. 310. 311. 312. 313. 314. 315. 316. 317. 318. 319. 320. 321. 322. 323. 324. 325. 326. 327. 328. 329. 330. 331. 332. 333. 334. 335. 336. 337. 338. 339. 340. 341. 342. 343. 344. 345. 346. 347. 348. 349. 350. 351. 352. 353. 354. 355. 356. 357. 358. 359. 360. 361. 362. 363. 364. 365. 366. 367. 368. 369. 370. 371. 372. 373. 374. 375. 376. 377. 378. 379. 380. 381. 382. 383. 384. 385. 386. 387. 388. 389. 390. 391. 392. 393. 394. 395. 396. 397. 398. 399. 400. 401. 402. 403. 404. 405. 406. 407. 408. 409. 410. 411. 412. 413. 414. 415. 416. 417. 418. 419. 420. 421. 422. 423. 424. 425. 426. 427. 428. 429. 430. 431. 432. 433. 434. 435. 436. 437. 438. 439. 440. 441. 442. 443. 444. 445. 446. 447. 448. 449. 450. 451. 452. 453. 454. 455. 456. 457. 458. 459. 460. 461. 462. 463. 464. 465. 466. 467. 468. 469. 470. 471. 472. 473. 474. 475. 476. 477. 478. 479. 480. 481. 482. 483. 484. 485. 486. 487. 488. 489. 490. 491. 492. 493. 494. 495. 496. 497. 498. 499. 500. 501. 502. 503. 504. 505. 506. 507. 508. 509. 510. 511. 512. 513. 514. 515. 516. 517. 518. 519. 520. 521. 522. 523. 524. 525. 526. 527. 528. 529. 530. 531. 532. 533. 534. 535. 536. 537. 538. 539. 540. 541. 542. 543. 544. 545. 546. 547. 548. 549. 550. 551. 552. 553. 554. 555. 556. 557. 558. 559. 560. 561. 562. 563. 564. 565. 566. 567. 568. 569. 570. 571. 572. 573. 574. 575. 576. 577. 578. 579. 580. 581. 582. 583. 584. 585. 586. 587. 588. 589. 590. 591. 592. 593. 594. 595. 596. 597. 598. 599. 600. 601. 602. 603. 604. 605. 606. 607. 608. 609. 610. 611. 612. 613. 614. 615. 616. 617. 618. 619. 620. 621. 622. 623. 624. 625. 626. 627. 628. 629. 630. 631. 632. 633. 634. 635. 636. 637. 638. 639. 640. 641. 642. 643. 644. 645. 646. 647. 648. 649. 650. 651. 652. 653. 654. 655. 656. 657. 658. 659. 660. 661. 662. 663. 664. 665. 666. 667. 668. 669. 670. 671. 672. 673. 674. 675. 676. 677. 678. 679. 680. 681. 682. 683. 684. 685. 686. 687. 688. 689. 690. 691. 692. 693. 694. 695. 696. 697. 698. 699. 700. 701. 702. 703. 704. 705. 706. 707. 708. 709. 710. 711. 712. 713. 714. 715. 716. 717. 718. 719. 720. 721. 722. 723. 724. 725. 726. 727. 728. 729. 730. 731. 732. 733. 734. 735. 736. 737. 738. 739. 740. 741. 742. 743. 744. 745. 746. 747. 748. 749. 750. 751. 752. 753. 754. 755. 756. 757. 758. 759. 760. 761. 762. 763. 764. 765. 766. 767. 768. 769. 770. 771. 772. 773. 774. 775. 776. 777. 778. 779. 780. 781. 782. 783. 784. 785. 786. 787. 788. 789. 790. 791. 792. 793. 794. 795. 796. 797. 798. 799. 800. 801. 802. 803. 804. 805. 806. 807. 808. 809. 810. 811. 812. 813. 814. 815. 816. 817. 818. 819. 820. 821. 822. 823. 824. 825. 826. 827. 828. 829. 830. 831. 832. 833. 834. 835. 836. 837. 838. 839. 840

search completed: August 12, 2002, 08:00:47

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 12, 2002, 07:51:08 ; Search time 59.07 seconds

(without alignments)
1679.176 Million cell updates/sec

Title: US-09-707-121-2

Perfect score: 4721

Sequence: 1 MFPLKDAEMKAFITFASALP.....DGGINKIKETGLITPSPI 893

Scoring table: HUSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 11073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :	Query	Score	Match	Length	DB	ID	Description
1: A.GeneSeq_032802.*	1: /SIDSL/qcqdala/hold-geneseq/geneseq-emb1/AA1980.DAT.*	4721	100.0	893	22	AA667396	Amino acid sequence
2: /SIDSL/qcqdala/hold-geneseq/geneseq-emb1/AA1981.DAT.*	2: /SIDSL/qcqdala/hold-geneseq/geneseq-emb1/AA1981.DAT.*	4721	100.0	893	22	AA667396	Novel human (NRP)
3: /SIDSL/qcqdala/hold-geneseq/geneseq-emb1/AA1982.DAT.*	3: /SIDSL/qcqdala/hold-geneseq/geneseq-emb1/AA1982.DAT.*	4690.5	99.4	892	22	AA662179	Human p100 protein
4: /SIDSL/qcqdala/hold-geneseq/geneseq-emb1/AA1983.DAT.*	4: /SIDSL/qcqdala/hold-geneseq/geneseq-emb1/AA1983.DAT.*	4690.5	99.4	892	22	AA662179	Human p100 protein
5: /SIDSL/qcqdala/hold-geneseq/geneseq-emb1/AA1984.DAT.*	5: /SIDSL/qcqdala/hold-geneseq/geneseq-emb1/AA1984.DAT.*	4690.5	99.4	892	22	AA662179	Human p100 protein
6: /SIDSL/qcqdala/hold-geneseq/geneseq-emb1/AA1985.DAT.*	6: /SIDSL/qcqdala/hold-geneseq/geneseq-emb1/AA1985.DAT.*	4690.5	99.4	892	22	AA662179	Human p100 protein
7: /SIDSL/qcqdala/hold-geneseq/geneseq-emb1/AA1986.DAT.*	7: /SIDSL/qcqdala/hold-geneseq/geneseq-emb1/AA1986.DAT.*	4690.5	99.4	892	22	AA662179	Human p100 protein
8: /SIDSL/qcqdala/hold-geneseq/geneseq-emb1/AA1987.DAT.*	8: /SIDSL/qcqdala/hold-geneseq/geneseq-emb1/AA1987.DAT.*	4690.5	99.4	892	22	AA662179	Human p100 protein
9: /SIDSL/qcqdala/hold-geneseq/geneseq-emb1/AA1988.DAT.*	9: /SIDSL/qcqdala/hold-geneseq/geneseq-emb1/AA1988.DAT.*	4690.5	99.4	892	22	AA662179	Human p100 protein
10: /SIDSL/qcqdala/hold-geneseq/geneseq-emb1/AA1989.DAT.*	10: /SIDSL/qcqdala/hold-geneseq/geneseq-emb1/AA1989.DAT.*	4690.5	99.4	892	22	AA662179	Human p100 protein
11: /SIDSL/qcqdala/hold-geneseq/geneseq-emb1/AA1990.DAT.*	11: /SIDSL/qcqdala/hold-geneseq/geneseq-emb1/AA1990.DAT.*	4690.5	99.4	892	22	AA662179	Human p100 protein
12: /SIDSL/qcqdala/hold-geneseq/geneseq-emb1/AA1991.DAT.*	12: /SIDSL/qcqdala/hold-geneseq/geneseq-emb1/AA1991.DAT.*	4690.5	99.4	892	22	AA662179	Human p100 protein
13: /SIDSL/qcqdala/hold-geneseq/geneseq-emb1/AA1992.DAT.*	13: /SIDSL/qcqdala/hold-geneseq/geneseq-emb1/AA1992.DAT.*	4690.5	99.4	892	22	AA662179	Human p100 protein
14: /SIDSL/qcqdala/hold-geneseq/geneseq-emb1/AA1993.DAT.*	14: /SIDSL/qcqdala/hold-geneseq/geneseq-emb1/AA1993.DAT.*	4690.5	99.4	892	22	AA662179	Human p100 protein
15: /SIDSL/qcqdala/hold-geneseq/geneseq-emb1/AA1994.DAT.*	15: /SIDSL/qcqdala/hold-geneseq/geneseq-emb1/AA1994.DAT.*	4690.5	99.4	892	22	AA662179	Human p100 protein
16: /SIDSL/qcqdala/hold-geneseq/geneseq-emb1/AA1995.DAT.*	16: /SIDSL/qcqdala/hold-geneseq/geneseq-emb1/AA1995.DAT.*	4690.5	99.4	892	22	AA662179	Human p100 protein
17: /SIDSL/qcqdala/hold-geneseq/geneseq-emb1/AA1996.DAT.*	17: /SIDSL/qcqdala/hold-geneseq/geneseq-emb1/AA1996.DAT.*	4690.5	99.4	892	22	AA662179	Human p100 protein
18: /SIDSL/qcqdala/hold-geneseq/geneseq-emb1/AA1997.DAT.*	18: /SIDSL/qcqdala/hold-geneseq/geneseq-emb1/AA1997.DAT.*	4690.5	99.4	892	22	AA662179	Human p100 protein
19: /SIDSL/qcqdala/hold-geneseq/geneseq-emb1/AA1998.DAT.*	19: /SIDSL/qcqdala/hold-geneseq/geneseq-emb1/AA1998.DAT.*	4690.5	99.4	892	22	AA662179	Human p100 protein
20: /SIDSL/qcqdala/hold-geneseq/geneseq-emb1/AA1999.DAT.*	20: /SIDSL/qcqdala/hold-geneseq/geneseq-emb1/AA1999.DAT.*	4690.5	99.4	892	22	AA662179	Human p100 protein
21: /SIDSL/qcqdala/hold-geneseq/geneseq-emb1/AA2000.DAT.*	21: /SIDSL/qcqdala/hold-geneseq/geneseq-emb1/AA2000.DAT.*	4690.5	99.4	892	22	AA662179	Human p100 protein
22: /SIDSL/qcqdala/hold-geneseq/geneseq-emb1/AA2001.DAT.*	22: /SIDSL/qcqdala/hold-geneseq/geneseq-emb1/AA2001.DAT.*	4690.5	99.4	892	22	AA662179	Human p100 protein

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	4721	100.0	893	22	AA667396	Amino acid sequence
2	4721	100.0	893	22	AA667396	Novel human (NRP)
3	4690.5	99.4	892	22	AA662179	Human p100 protein
4	4690.5	99.4	892	22	AA662179	Human p100 protein
5	4690.5	99.4	892	22	AA662179	Human p100 protein
6	4690.5	99.4	892	22	AA662179	Human p100 protein
7	4690.5	99.4	892	22	AA662179	Human p100 protein
8	4690.5	99.4	892	22	AA662179	Human p100 protein
9	4690.5	99.4	892	22	AA662179	Human p100 protein
10	4690.5	99.4	892	22	AA662179	Human p100 protein
11	4690.5	99.4	892	22	AA662179	Human p100 protein

ALIGNMENTS

Result	1
AA667396	standard: Protein: 893 AA.
AA667396	13-NOV-2001 (first entry)
AA667396	Human: protein kinase; cancer; immune disease; cardiovascular disease; brain disease; neuronal disease; Alzheimer's disease; chromosome 4; Parkinson's disease; multiple sclerosis; metabolic disorder; peripheral nervous system disease; amyotrophic lateral sclerosis; infection; ocular disease; migraine; pain; sexual dysfunction; mood disorder; attention disorder; cognition disorder; hypotension; hypertension; psychotic disorder; dyskinesia; transplant rejection.
AA667396	Homo sapiens.
AA667396	MO200166594-A2.
AA667396	13-SEP-2001.
AA667396	02-MAR-2001; 2001WO-US06838.
AA667396	06-MAR-2000; 2000US-0187150.
AA667396	29-MAR-2000; 2000US-0193404.
AA667396	13-NOV-2000; 2000US-0247013.
AA667396	(SUGG-) SUGEN INC.
AA667396	Plozman CB, Whyte D, Manning G, Sudarsanam S, Martinez R;

Consensus protein:
Consensus sequence
KAT neuronal prote
S cerevisiae apc p
protein involved i
SHPP. Yeast sp.
Human protein sequ
Amino acid sequen
Wheat putative car
corn putative carb
Consensus sequence
Human STEK3 protei
Human pan-s/1k 1A
Human pan-s/1k 1B
Arabidopsis thalia
C albicans apoptos
Arabidopsis thalia
Arabidopsis thalia
T60K-20 protein se
CDK6 K10C mutant
Yeast protein kind
Drosophila melanog
Arabidopsis thalia
Arabidopsis thalia
Soybean putative c
Rat pan-s/1k 1recp
A. thaliana MAP ki
A. thaliana MAP ki
Human kinase (pkin
Human polypeptide,
Zea mays protein t
Zea mays protein t
Zea mays protein t
Soybean putative c

CC as a hybridisation probe for screening libraries, assessing gene
 CC expression patterns and in NHP regulation.

XX Sequence 893 AA:

Query Match 100.0%; Score 4721; DB 22; Length 893;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 893; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MEPLDAMGAAATFASALPHDVCSNGLPLPNSIKILGRQILKTTTHRLCYVDIS 60
DB 1 mtlpldaemgaatffasalphdvcsnqlpltpnsikilgrtqltktlthrpilcyvd 60
QY 61 RKKHRLVVAHCHRSLEDLIRKKPVCSSTVLCAIEVLOGIÖYMKHGIHVHRAISPH 120
DB 61 rkkhrlvvahchrsledlirkkpvcstvlclatievlogiygmkhgihvraalsph 120
QY 121 NILLDRKCHIKLAKFGLYHMTAHGDVDFPIGYPYSLAEVLAQIGFTTHMPSKKPLP 180
DB 121 nilldrkchiklakylyhmtahgdvdfpiggypslapevlaqigfttthmpskkplp 180
QY 181 SGPKSDVWSLGLIFELCVGRKLFOSLDSERLKLTLTLCVDTLIVLAEHGCGLDIK 240
DB 181 sgpkdsvwsllglifelcvgrklfoslserlkltltlcvdttlivaehgcldiik 240
QY 241 ELPEIVIDLNLKLTFFHPSKRPTECLMKDKVESEVSPLEYPETPASFSSSLGADLT 300
DB 241 elpeividlnlkltffhpskrptelcmkdkevevspleypetpafssslgadt 300
QY 301 LPEDISQICKDINDYLAERSIEEYVYLWCLAGDLEKLVNKEITRSKPPICLPLELF 360
DB 301 lpedisqickdindylaesieeyyllwclagdlekelvnyketrskppiclpelf 360
QY 361 EDGESFQUGROSSSLDQTTVTLSCQLKRNKLDVGSSEAFYLLDDDSNLPHSNMNL 420
DB 361 edgesfqugrossslldqttvtlscqlkrrnkldvgsseafylldddsnlphsnm 420
QY 421 SAAATPLITTRKDEYQUNRIILFDRLCAKPYKKKNQWKFARVDIPLMGLTMAAL 480
DB 421 ssaatplitrkdeyqnriilfdrlcakpykkknqwkfarvdipmlgltmaali 480
QY 481 GVEGAIHAKYDAIDKDTPLPTLRQILEVDLPRCHQYDELLSSPEGHAKFRRLKAWVSH 540
DB 481 gvegaihakydaidkdtplptlrqilevdprchqydelsspeghakfrvllkawvsh 540
QY 541 DLVYWGJDSLCAPRTIYLFNNEALAYACMSAFIRKYLAFNFKNSHVTQRYLVFSQM 600
DB 541 dlvywgjdsldcaprtiylfnnealayacmsafrkylafnflkshvltqyrlvtsqm 600
QY 601 IAFHDELSNHCNFGFIDLYALFWELCTMETHVPLERJPHWOTLLIGNSSPFCIGV 660
DB 601 iafhdeelsnhcnfgfidlyalfwelctmethvplerkjphwotllignsfpfcigv 660
QY 661 AIIQQLRRLIANGNCTNELLFSDLPETIDFRQVRSINLFCWTPRSATYRHOAPKPS 720
DB 661 aiiqqlrrliangnctnellfspdpetidfrqvrsinlfcwtpksayrqbapkpks 720
QY 721 SSSSGRSAPYSACPRPPKTULSRESIFLNDLKSESPKISABDLIDLTLVTGHR 780
DB 721 ssssgrsapyisacpprpktdlresiflndlksevspkisabdlidlclvtghr 780
QY 781 KIPSKRTKSSKPKLIVDILKNSHDFIRGHISGSINIPESAAATAGGELTGGYTAMLONF 840
DB 781 kipskrtksskpkllvdlrnsedfirghisgsinipisaatagaeltgpytamlonf 840
QY 841 KCKVIVIVCHVAKHTAEFAAHVKMKYPRICILINGINKIKTGLTIPSPPI 893
DB 841 kckviviwhvakhtaefaaahvkmypricilidgainkikpqltltspspi 893

```

RESULT 3
 AAB62179

TD AAB62179 standard; Protein: 892 AA.

XX AAB62179;

XX 11-JUN-2001 (first entry)

XX Human p100 protein.

DE
 XX Rbb; Rho; GTPase; pharmacological; cancer; anti-HIV; tuberculosis;
 KW protozoacide; antidiabetic; neurotropic; neuroprotective; dermatological;
 KW antiporlatic; antiinflammatory; antiallergic; antipruritic; cytosatic;
 KW antibacterial; gynecological; antiatherosclerotic; gene therapy; human;
 KW p100; p95; p60; p45; p25; endocytic trafficking; GTPase effector.

XX Homo sapiens.

XX W0200120022-A1.

XX 22-MAR-2001.

XX 18-SEP-2000; 2000WO-EP09130.

XX 16-SEP-1999; 99EP-0118385.

XX (PLAC) MAX PLANCK GES FORDERUNG WISSENSCHAFTEN.

XX Nielsen E, Christophoridis S, Murphy C, Zerial M, De Renzis S;

XX WPI: 2001-257888/26.

XX N-PSDB: AAF57407.

PT Use of effectors of GTPase as target in a in vitro/vivo assay for
 PT detecting substances for prophylaxis, treatment of cancer, cell
 PT migration disorders, e.g. Alzheimer's, infectious diseases, diabetes,
 PT atherosclerosis

XX Disclosure: Page 66-70; 76pp; English.

XX The invention relates to the use of effectors/regulators for Rab and Rho
 CC GTPases in in vitro or in vivo assays. The method is useful for detecting
 CC substances useful as pharmaceutical agents for the prophylaxis or
 CC treatment of cancer and other proliferative, invasive or cell migration
 CC disorders such as endometriosis, atherosclerosis, inflammatory and
 CC allergic diseases, infectious diseases, diabetes, Alzheimer's disease and
 CC skin repair diseases such as psoriasis. The infectious diseases include
 CC AIDS, tuberculosis, pseudotuberculosis, chloeria, gastroenteritis, enteric
 CC fever, malaria, typhus, diseases caused by pathogens such as listeria,
 CC Mycobacterium, Stephylococcus, Toxoplasma, Trypanosoma, Salmonella,
 CC Legionella, Leishmania, Coxiella, Shigella, Yersinia, Neisseria, Vibrio,
 CC Bartonella. The cancer includes benign tumor, malignant tumor, carcinoma,
 CC leukemia, glioma or a neuroblastoma, in particular lung carcinoma,
 CC osteosarcoma, lymphoma, breast, bile, intestine, kidney, ovary, stomach,
 CC brain, prostate, liver and every tumor that invades other tissues and
 CC organs distinct from its site of origin. The assay is highly sensitive
 CC and advantageous in the selectivity of the targets. The present sequence
 CC represents the human p100 protein. A multiprotein complex including p100,
 CC p95, p60, p45, p25 (sequences AAB62176-180) acts as a GTPase effector/
 CC regulator and has the function of endocytic trafficking.

XX Sequence 892 AA:

Query Match 99.4%; Score 4690.5; DB 22; Length 892;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 889; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

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QY 1 MEPLDAMGAAATFASALPHDVCSNGLPLPNSIKILGRQILKTTTHRLCYVDIS 60
DB 1 mtlpldaemgaatffasalphdvcsnqlpltpnsikilgrtqltktlthrpilcyvd 60
QY 61 RKKHRLVVAHCHRSLEDLIRKKPVCSSTVLCAIEVLOGIÖYMKHGIHVHRAISPH 120
DB 61 rkkhrlvvahchrsledlirkkpvcstvlclatievlogiygmkhgihvraalsph 120

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QY	568	ACWAAFLPEKTLVYVPEFLAKDQNSINVLQEVLTAFESQVLAIAHDEPELSNHLNEIGCFIPDLVATVMP	627
Db	301	acmsaflpkyllynlfkksnshvqelylvlsqgmatahpeishnlneiqfipdlvaylpwf	360
QY	628	LIMETVPEPLAKLIFHIMDTLLGNSSSPFCIGVALILO-LDRORLIANGFNECTILFSDLP	686
Db	361	lmtlthvtrphkklthlwdtlllgnssstpicqssussagcgytmanqfneclllfssdlp	420
QY	687	EIDIEKCVRESINLFWTPKSAATVYKQIAOPPEKFSDDSCGKSSADVPFAKCPDPKPTDLS	746
Db	421	eidercvresinlfcwlypkasatyrqhaqppkssdsagysapaylsaeppdktdls	480
QY	747	RESIFLMDLKSSESPRISADLLIDIGELVYTGAFKTPSKRTSSKPKLLVYVIRKSEPI	806
Db	481	resifplndlksevsprisaedllidcelvtvgnlkkpskklsskpklllvddlrnsedll	540
QY	807	RGHISGSINLPEASAPFAEGELTGGTYTAMLQWPKGVIVIGVHAKRTAEFAALVYMK	866
Db	541	rghisgsinlprisaatacgeqltqgpytlamlqfkavlvlyvhwakhaefaaahlvxmk	600
QY	867	YPRKFIIDGGINKIKPTGLTITVSPQI	893
Db	601	yprcfllidgqinkikipqlllpspqf	627
RESULT 5			
AAU17261	1D	AAU17261 standard; Protein: 436 AA.	
AAU17261	AC		
AAU17261	XX		
DI	07-NOV-2001	(first entry)	
DE		Novel signal transduction pathway protein, Seq ID 825.	
XX			
XX		Neuroprotective; cytosolic; dermatological; immunosuppressive; tumour;	
XX		antitumour; anti-HIV; antibacterial; antiinflammatory; cancer;	
XX		immune system disorder; rheumatoid arthritis; inflammatory condition;	
XX		organ transplant rejection; infection; hepatitis C; blood disorder;	
XX		sickle cell anaemia; hyperproliferative disorder; Gaucher's disease;	
XX		neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;	
XX		chromosomal abnormality; down syndrome; ischaemia; renal disorder;	
XX		cardiovascular; respiratory; wound healing; endocrine; Addison's disease;	
XX		reproductive system; gastrointestinal; liver disorder; AIDS;	
XX		acquired immune deficiency syndrome.	
OS		Homo sapiens.	
XX		MO200154733-AL.	
PN			
XX		02-AUG-2001.	
FD			
XX		17-JAN-2001; 2001WO-0501312.	
XX			
XX	31-JAN-2000;	2000US-0179065.	
PR	04-FEB-2000;	2000US-0180628.	
PR	24-FEB-2000;	2000US-0184664.	
PR	02-MAR-2000;	2000US-0186350.	
PR	16-MAR-2000;	2000US-0198474.	
PR	17-MAR-2000;	2000US-0190076.	
PR	18-APR-2000;	2000US-0198124.	
PR	19-MAY-2000;	2000US-0205515.	
PR	07-JUN-2000;	2000US-0209467.	
PR	28-JUN-2000;	2000US-0214885.	
PR	30-JUN-2000;	2000US-0215135.	
PR	07-JUL-2000;	2000US-0216647.	
PR	07-JUL-2000;	2000US-0216880.	
PR	11-JUL-2000;	2000US-0217487.	
PR	11-JUL-2000;	2000US-0217496.	
PR	14-JUL-2000;	2000US-0218290.	
PR	26-JUL-2000;	2000US-0220963.	
PR	26-JUL-2000;	2000US-0220964.	
PR	14-AUG-2000;	2000US-0224518.	

[illegible]

PR 09-JUL-2000; 2000US-0598042.
 PR 19-JUL-2000; 2000US-0620312.
 PR 03-AUG-2000; 2000US-0653450.
 PR 14-SEP-2000; 2000US-0662191.
 PR 19-OCT-2000; 2000US-0693036.
 PR 29-NOV-2000; 2000US-0727344.

XX (HYSEQ-) HYSEQ INC.

PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman F, Xu C, Xue AJ, Yane Y, Zhang J;
 PI Zhao QA, Zhou P, Gocorlich R, Ormanac RT;

DR WPI: 2001-442253/47.
 DR N-PSDB: AA159937.

PT Novel nucleic acids and polypeptides, useful for treating disorders
 PT such as central nervous system injuries -

XX Example 2: SEQ ID NO 5712: 10078pp; English.

CC The invention relates to human nucleic acids (AA157798-AA161369) and
 CC the encoded polypeptides (AA157842-AA161421) with nootropic,
 CC immunosuppressant and cytoskeletal activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localized neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilization of the activities such as: immune system suppression,
 CC Activation/inhibition activity, chemotactic/chemokinetic activity, hemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukemias and
 CC C.N.S disorders.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.

XX Sequence 462 AA:

Query Match 46.5%; Score 2194.5; DB 22; Length 462;
 Best Local Similarity 91.5%; Pred. No. 3,66-199;

Matches 418; Conservative 9; Mismatches 29; Indels 1; Gaps 1;

DB 200 GRKLEFSDISRLKRLTLTPVVDTLVLAEEGGLIKLPTVIDLKKCLTHPS 259

DB 1 GKLLISIDISRLKRLTLTPVVDTLVLAEEGGLIKLPTVIDLKKCLTHPS 60

DB 260 KRPTEDELMKRVSEVSEPLYPETPKPASPSSSLKADLTPEISQCDINDDYAE 319

DB 61 KRPTEDELMKRVSEVSEPLYPETPKPASPSSSLKADLTPEISQCDINDDYAE 120

DB 320 RSIEEYVYLMVLAEEGGLIKLPTVIDLKKCLTHPS 379

DB 121 RSIEEYVYLMVLAEEGGLIKLPTVIDLKKCLTHPS 180

DB 380 TPTLSICQIRNKLKGVGEAFPLLEDVQSLPHSNNSNNEAATLPLIREQTEYQ 438

DB 181 hwdlvmpakkklercwrgrsllpiklmsllpysnsnneaaalplllirekdeyq 240

DB 439 LMRLLFDELLKAVPYKKKQIWEKRVDPPLMRSLTMAALIGVCATIAKADAIKQTP 498

DB 241 LMRLLFDELLKAVPYKKKQIWEKRVDPPLMRSLTMAALIGVCATIAKADAIKQTP 300

DB 499 IFTDRQLEVDIPRQHQVDLSSPESGAKFRRLKAWVSHBDLYWQGLDSICAPFLYL 558

DB 301 IFTDRQLEVDIPRQHQVDLSSPESGAKFRRLKAWVSHBDLYWQGLDSICAPFLYL 360

DB 559 NNNNNALAACSAAPKRYLYNFKKNSHVUQELTVSSQMIARDPRLSHLNEIGFI 618

DB 361 nlnnealvaymsatipkylyntfklkdnshvqeylvvisgmatahdpeishlnleigfi 420

QY 619 PDLYAIPWFLTMFTNPEFLKIFHLWDLTGNSSP 655
 DB 421 pdlyaipwfltmftnpeflkifhlwdltgnspp 457

RESULT 7

AB060366
 ID AB060366 standard; Protein; 840 AA.

AC AB060366;

DT 26-MAR-2002 (first entry)

DE Drosophila melanogaster polypeptide SEQ ID NO 7890.

KW Drosophila; developmental biology; cell signalling; insecticide;

OS Drosophila melanogaster.

PN W0200171042-A2.

PD 27-SEP-2001.

PF 23-MAR-2001; 2001WO-0509231.

PR 23-MAR-2000; 2000US-191637P.

PR 11-JUL-2000; 2000US-0614150.

PA (PEKE) PE CORP NY.

PI Venter JC, Adams M, Li FWD, Myers RW;

DR WPI: 2001-656860/75.

DR N-PSDB: AB104469.

PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -

XX Disclosure: SEQ ID NO 7890: 21pp + Sequence Listing; English.

CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and

CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB101840-AB116175), expressed DNA

CC sequences (AB101840-AB116175) and the encoded proteins

CC (AB101840-AB116175).

CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WPI
 CC at http://wipo.int/pub/publist/wipo_sequences.

XX Sequence 840 AA:

Query Match 37.6%; Score 1775.5; DB 22; Length 840;
 Best Local Similarity 42.3%; Pred. No. 6,16-159;

Matches 388; Conservative 133; Mismatches 277; Indels 119; Gaps 13;

DB 5 KDAEGAFTEFASALPHVCGSNGCPIIPNSIKILGHPULKTTIRPLCYVPIISGXH 64

DB 8 recticavlitaklhpqdvgsnqpltpnsiallyaqkikeqdcnlydvitqkh 67

DB 65 ERLVVAEHCERSLEDLREKRPVSGSTVICIAFEVLOGIYNNKRGIVHKAISPHNILL 124

DB 68 ertlvseaylqsltdymrhpplaiqlrllyqvaqvlvshrlvahnvepkhlll 127

DB 125 DRKG-HIKLAFGLYHMKABGDWDVPIGYTSYIAPVIAOGIFKTTIDHPSKAPLPSCP 183

DB 128 ssdqrvkllyngdthmtkgaayvipipnrlfymaperll-----qldany 174

Db 144 lltvqtpwmmapevlltqrqyss:-----kvdwsivqvllyelltqapllp 190

QY 206 SLDISEKRLKLLTLKCYVDLIVLAEEHGCIDILKEPTEVYI-----247

Db 191 qad-----lpaftqdevdqlilvfk-----lpsdelpkrlpdlpaelfrlkrtrlpips 242

QY 248 -----DLNKKCLTFHPSKRP---TPDELKMDKVF 273

Db 243 ncsseklklkclnkdpkskrpsatakeellnlpwf 278

RESULT 13

AAG67543

ID AAG67543 standard; Protein: 239 AA.

XX AC AAG67543;

XX 26-NOV-2001 (first entry)

DE Consensus sequence of an eukaryotic protein kinase domain.

XX Human: kinase; 2504; 15977; 14760; cellular proliferative disorder;

KW cellular differentiative disorder; neural disorder; immune disorder;

KW cardiovascular disorder; liver disorder; skin disorder;

KW skeletal muscle disorder; bone metabolism; cardiovascular disorder;

KW viral disease; pain; metabolic disorder; blood vessel disorder;

XX hepatic disorder; liver disorder.

OS Synthetic.

XX W0200164905-A2.

FN 07-SEP-2001.

XX 28-FEB-2001; 2001WO-US06525.

XX 29-FEB-2000; 2000US-0186061.

XX (MILL.) MILLENNIUM PHARM INC.

PA (MILL.) MILLENNIUM PHARM INC.

PI Olandt PJ, Kapeller-Libermann R, Meyers KA;

XX WPI; 2001-570697/64

DK New protein kinase family polypeptides for treating hematopoietic

PT neoplastic disorders, immune disorders, cardiovascular disorders and

XX disorders of blood vessels

XX Disclousure: Fig 6A; 145pp; English.

XX The present sequence represents a consensus protein kinase domain.

CC The specification describes human kinases 2504, 15977 and 14760. The

CC kinase polypeptides and polynucleotides are used to treat cellular

CC proliferative or differentiative disorders, neural disorders, immune

CC disorders, cardiovascular disorders, liver disorders, skin disorders and

CC skeletal muscle disorders. They may also be used for controlling

CC disorders associated with bone metabolism, cardiovascular disorders,

CC viral diseases, pain or metabolic disorders, blood vessel

CC disorders, and hepatic or liver disorders.

XX Sequence 239 AA;

SQ

Query Match 6.28; Score 294.5; DB 22; Length 219;

Best Local Similarity 35.1%; Pred. No. 3,5e-19;

Matches 84; Conservative 37; Mismatches 83; Indels 35; Gaps 8;

QY 35 SIKILAR-----FQIIKITHTPRLCYVDISRCRHEFLVAVAHCE-RSLIEDLRERK 86

Db 27 aklikkkskslrlqilklrlshpnlvrlqvfedddhlylvmeymcqgdlfdylrrng 86

QY 87 PVSCTVLCAFEVLQGIQYNNKKGIVHRAISPENIILDRKCHIKLARFGYHMTAGDD 146

Db 87 plsteakakktialqilrtleylhnqvthrldkpenllldenqvkladqlarll---ek 144

QY 147 VDFPICPST-LADPVLQAGIFKTTDHPMSKKPLPSGPKSWSLGILIFELCVGKKILY 205

Db 144 lltvqtpwmmapevlltqrqyss:-----kvdwsivqvllyelltqapllp 190

QY 206 SLDISEKRLKLLTLKCYVDLIVLAEEHGCIDILKEPTEVYI:MKCLTFHPSKRP 264

Db 191 qad-----lpaftqdevdqlilvfk-----lpsdelpkrlpdlpael-frlkrtrlp 239

RESULT 14

AAR98226

ID AAR98226 standard; Protein: 779 AA.

XX AC AAR98226;

XX 23-SEP-1996 (first entry)

DE Rat neuronal protein kinase MARK-1.

XX Neuronal protein kinase; NPK; microtubule associated protein;

KW MAP; tau protein; phosphorylation; NPK inhibitor; Alzheimer disease;

KW cancer; therapy; diagnosis.

XX Rattus norvegicus.

XX W09613592-A2.

PN 09-MAY-1996.

PD 30-OCT-1995; 95WO-EP04258.

PF 28-OCT-1994; 94EP-0117122.

XX (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.

PA BERNAT J, DREWES G, MANDELKOW E;

XX WPI; 1996-251461/25.

DK DNA encoding neuronal protein kinase (NPK) - useful for identifying

PT NPK inhibitors for treatment of Alzheimer's disease and cancer.

XX Claim 1; Page 44-45; 77pp; English.

XX A novel rat neuronal protein kinase (AAR98226), designated NPK MARK-1,

CC is capable of phosphorylating a KXS sequence motif in tau protein

CC and microtubule associated proteins MAP4, MAP2 and MAP2c (see also

CC AAR98229-39 and AAM00850-54), causing their dissociation from

CC microtubules. Phosphorylation of human tau Ser 262 is indicative of the

CC onset of Alzheimer's disease. MARK-2 is the product of a cDNA clone

CC obtd. from a rat brain cDNA library by screening with probes derived

CC from pig brain peptide sequences (see also AAR98240-50). Another NPK,

CC MARK-2 (AAR98227), was similarly isolated. Inhibitors (e.g. antibodies)

CC of NPKs are used to treat Alzheimer's disease and cancer. NPKs are

CC themselves used for in vitro diagnosis and/or monitoring of

CC Alzheimer's disease and cancer.

XX Sequence 779 AA;

SQ

Query Match 5.98; Score 280; DB 17; Length 779;

Best Local Similarity 25.1%; Pred. No. 6,1e-17;

Matches 112; Conservative 66; Mismatches 156; Indels 108; Gaps 17;

QY 31 LTPNSI-KILGRFOLKITHTPRLCYVDISRCRHEFLVAVAHCEERSIDLRERKPS 89

Db 82 lnpstqklrtrevrlmkllnlpnlvklrtvleoktlylvmeysqdevvdyvahrnk 141

QY 90 CSTVLCAFEVLQGIQYNNKKGIVHRAISPENIILDRKCHIKLARFGYHMTAGDDVP 149

Genome version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 12, 2002, 04:21:57 ; Search time 2032.31 Seconds
(without alignments)
17811.669 Million cell updates/sec

Title: US-09-707-121-1
Perfect score: 2682
Sequence: 1 atgttcccttgaagaaagc.....tccatctctcaataataga 2682

Scoring table: 10BENTY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues
Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_estlum:*
3: em_estlu:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: qb_est1:*
10: qb_est2:*
11: qb_hic:*
12: qb_qss:*
13: em_qss_hum:*
14: em_qss_inv:*
15: em_qss_pln:*
16: em_qss_vrl:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query length	DB ID	Description
1	1461.4	54.6	2428	11 AF161420	AF161420 Homo sapi
2	577.4	21.5	812	10 BG204777	BG204777 RST24192
3	574.2	21.4	583	9 AW500718	AW500718 UT-HF-BNO
4	524.2	19.5	625	9 BB65071	BB65071 BB65071
5	523.8	19.5	616	9 AV716189	AV716189 AV716189
6	521	19.4	627	9 BB659632	BB659632 BB659632
7	510	19.0	874	10 BF676470	BF676470 603084269
8	500	18.6	572	10 BM087952	BM087952 501280 MA
9	499	18.6	507	10 BF931516	BF931516 IL2-N1020
10	495.8	18.5	582	10 BF682521	BF682521 463631 MA
11	493	18.4	573	9 AV615075	AV615075 AV615075
12	461.8	17.2	799	10 BE541855	BE541855 601064138
13	442.8	16.5	701	9 BB513783	BB513783 BB513783
14	427.6	15.9	482	10 BP906385	BP906385 RC4-OT008
15	416.2	15.5	421	9 AA663589	AA663589 ac71e02.s
16	406	15.1	455	9 AW437042	AW437042 77775 MAR
17	382.2	14.3	532	10 B1460474	B1460474 603200972

18	377.8	14.1	715	10 B1518420	B1518420 603062125
19	370	13.8	453	10 H16878	H16878 ym44137.t1
20	369.2	13.8	472	9 AA488854	AA488854 UT1-M-HR2
21	368.8	13.8	501	10 H09671	H09671 Y199406.t1
22	361.8	13.5	415	10 H84971	H84971 Y889407.t1
23	360.2	13.4	514	10 N50504	N50504 Y889407.t1
24	355.2	13.2	1047	11 AK007218	AK007218 Mus. muscu
25	354.6	13.2	544	10 HM183100	HM183100 1450001.Y
26	352.8	13.2	468	9 AA809486	AA809486 db85c11.s
27	349	13.0	349	10 Z44040	Z44040 Hs1161021.n
28	349	13.0	449	10 R56761	R56761 Y995104.t1
29	347.2	12.9	464	10 H16267	H16267 ym22a05.t1
30	347	12.9	349	10 Z44727	Z44727 Hs273071.n
31	330.4	12.1	650	9 BB584530	BB584530 BB584530
32	325.6	12.1	670	9 BB637890	BB637890 BG478490
33	319	11.9	444	9 AA363673	AA363673 EST74145
34	315	11.7	504	10 R91239	R91239 YP4411.t1
35	308.6	11.5	664	9 BB661831	BB661831 BB661831
36	297.2	11.1	313	10 BF931560	BF931560 112-N1020
37	292.8	10.9	437	10 N58608	N58608 y65609.t1
38	289	10.8	300	9 AA852911	AA852911 NM183a01
39	287	10.7	609	10 B1186076	B1186076 UNL-p-FN-
40	286	10.7	609	10 H1182055	H1182055 UNL-p-FN-
41	284.4	10.6	597	10 BG208487	BG208487 RST27989
42	282.4	10.5	604	9 AV869953	AV869953 AV869953
43	282	10.5	399	10 T95749	T95749 y64012.t1
44	279	10.4	457	9 A1235562	A1235562 RST232124
45	276	10.3	714	9 AV715003	AV715003 AV715003

ALIGNMENTS

RESULT	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	TITLE	JOURNAL	FEATURES
1	AF161420	Homo sapiens HSPC302 mRNA, partial cds.	AF161420	AF161420.1	GI:6841253	human.	human.	Ye, M., Zhang, Q. H., Zhou, J., Shen, Y., Wu, X. Y., Guan, Z. Q., Wang, L., Fan, H. Y., Mao, Y. F., Dai, M., Huang, Q. H., Chen, S. J., and Chen, Z.	Submitted (14-MAY-1999) Shanghai Institute of Hematology, Shanghai Second Medical University, Rui-Jin Hospital, 197 Rui-Jin Road 11, Shanghai 200025, P. R. China		location/Qualifiers 1..2428 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="CRFBM02" /cell_type="cd4+ stem cell" /tissue_type="blood" <1..1524 /codon_start=1 /product="HSPC302" /protein_id="AA029890.1" /db_xref="GI:6841253" /translation="LNRKIKDVGGEAFYPLIEDDSNLPHSNNSLSAATPLIIR EKTEFYDNNKILLDLLKAYPRKNDIMKEAYVDITIMKGLTKALGIVGATIAK YVADIDKPIPIPIKOTESGSSLSVVEILLISPEGIKAEKRRVIRAWVSIVDLYWOG LDSLCAPFLLNNENLAVACMSAFPKYLYNFFIKNSHIVDFEITVLSUNNAHD PELSNHNENIGFIPDLVAIPWLTMTFTVHTVTKIKIFELMTITLLCNSSPEFCIGSSNS

LOCUS	AV716189	616 bp	mRNA	linear	EST 11-OCT-2006
DEFINITION	AV716189	DCB Homo sapiens cDNA clone (BCBA05.5')	mRNA sequence.		
ACCESSION	AV716189				
VERSION	AV716189.1	GI:10797706			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	Xu, X., Gu, J., Liu, F., Qu, J., Zhao, M., Li, Y., Huang, Q., Zhou, J., Song, H., Gu, Y., Yang, Y., Gao, C., Xiao, H., Li, N., Qian, B., Gao, X., Cheng, Z., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, Y., Cheng, Z., and Han, Z.				
TITLE	Homo sapiens DCB clones				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Zeyuan Han Chinese National Human Genome Center at Shanghai 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China Tel: 86-21-50801919(ext.45) Fax: 86-21-50801922 Email: hanzq@chc.sh.cn This clone is available at CHGC in Shanghai.				
FEATURES	source				
	1..616				
	/organism="Homo sapiens"				
	/db_xref="taxon:9606"				
	/clone="1XBCBA05"				
	/clone_1lb="DCB"				
	/cell_type="dendritic cells"				
	/dev_stage="mature"				
	/lab_host="BM25.R"				
	/note="Vector: pTRIPLEX2; Site_1: stIIA; Site_2: stIIb"				
BASE COUNT	164 a 152 c 127 g 173 t				
ORIGIN					
Query Match	19.5%	Score 523.8;	DB 9;	Length 616;	
Best Local Similarity	91.3%;	Pred. No. 86-131;			
Matches	589;	Conservative	0;	Mismatches 2;	Indels 54;
				Gaps	1
QY	1898	atgttcttctcatcacaacaaatttccacgtctgacatcacttactactatgaattct	1957		
DB	26	ATGCATTTCCATACACAAAATTTAGACCTCTGSGATACCTTACTTATGGCAATTCCT	85		
QY	1958	cttcccaattctgatatgaattacgaattcttcaacacatctgcagacgcgcgttctggcta	2017		
DB	86	CTTTCGCATTTCTGTATGAGTAGCAATTTCTTCACACAGCTCGGGACCGCGCTTTGGCTA	145		
QY	2018	atggctttaatgaatgataattcttctctctccgatttaccagaatttgacattgaacgt	2077		
DB	146	ATGGCTTTAATGAGTATTTCTTCTTCTTCATTTTACCAAGAAATTCACATTGAACGCT	205		
QY	2078	gattagagaatctatcaacacgatttcttctggaactctaaagtgctacttacaagacg	2137		
DB	206	GTGTGAGAAATCTATCAACGCTGTTTGTGGACTCTCTAAAGTGTACTTACAGACAC	265		
QY	2138	atgctcaaccttcaagacatctcttgcacacagatggaagatctggacaccttatt	2197		
DB	266	ATGCTCAACCTTCAAAAGCGCATCTTGTGACAGACAGTGGACGCAAAATTCGCGACCTATT	325		
QY	2198	tctctgctgaattatctcaagctctctcgaagagaaatctgccaagaaatccatccattaa	2257		
DB	326	TCTTCTACTGAGTGTCACATCTCTCCAAAACAGATTTGTCAACAGCAATCCATCCATTAA	385		
QY	2258	atgaccttgaattcgaagatcagacacgaattctgaagaagacctgaattgatttgg	2317		
DB	386	ATGACCTGAAGTCACAGATATCACCGACGGAATTTGACAGACAGGACCTGATTGACTTGTC	445		

QY	2318	acgtcaagatgaagagacacttcaaacaccccaagaaacaaagatcgaataaacca	2377
DB	446	AGGTCACAGTACAGAGCCACCTTCAAAACACCCAGACAG-----	484
QY	2378	agctctcagtgatcatccgaataataaagacttattctgtgacatlltcaagaa	2477
DB	484	-----GACTTATTGCTGGTCACATTTCAGGAA	511
QY	2478	gcatacaatccatccatgaatgactgacttcaactgtgaaagaaagacatgcccaagaccc	2497
DB	512	GCATCAACATTCGATTCAGTACTGCTTACTGTCAGAAAGAAATCTTATCTCAAGAGAGCTT	571
QY	2498	aacactgatactctcaagaacttcaaaagaaagatattgtatctatctg	2542
DB	572	ACACTGTATGCTCCAGAACTTCAAGAGGAAGATATTGTATCTATCG	616
RESULT	6		
LOCUS	BR659632	627 bp	mRNA linear EST 26-oct-2001
DEFINITION	BR659632 RIKEN full-length enriched, 13 days embryo lung mus		
ACCESSION	BR659632		
VERSION	BR659632.1	GI:16491453	
KEYWORDS	EST.		
SOURCE	mouse mouse.		
ORGANISM	Mus musculus		
REFERENCE	Eutheria: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Mus: 1 (bases 1 to 627)		
AUTHORS	Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanada,K., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sodabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toyota,T., Muramatsu,M. and Hayashizaki,Y.		
TITLE	RIKEN Mouse ESTs (Arakawa,T., et al. 2001)		
JOURNAL	Unpublished (2001)		
COMMENT	Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Shohiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 240-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@sc.riken.go.jp, URL: http://genome-res.riken.go.jp/ Carninci,P., Shibata,Y., Hayashi,N., Suahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap trapper selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res., 10 (10), 1617-1630 (2000) Maqil,K., Fujisake,S., Inoue,K., Toyawa,Y., Iizawa,M., Ohara,F., Watabiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kita,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multipipillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Konno,H., Fukushii,Y., Shibata,K., Itoh,M., Carninci,P., Suahara,Y. and Hayashizaki,Y. Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res., 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamazaki,T., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y. Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome, 12, 673-677 (2001) Please visit our web site (http://genome-res.riken.go.jp) for further details. e mouse tissues.		

QY 2045 tctcatttaccagaatgacattgaacgtctgtgaagaatctatcaacctgttt 2104
 |||||||
 Db 257 tcttcgatttaccagaatgacattgaacgtctgtgaagaatctatcaacctgttt 316
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 QY 2105 gtttgaacttctaaagttaacttacttacttacttacttacttacttacttactt 2164
 |||||||
 Db 317 gtttgaacttctaaagttaacttacttacttacttacttacttacttacttactt 376
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 QY 2165 acagatgag 2224
 |||||||
 Db 477 acagatgag 436
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 QY 2225 acagatgag 2284
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 Db 437 acagatgag 496
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 QY 2285 gatttgcag 2344
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 Db 497 gatttgcag 555
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 QY 2345 caccacgaagaagaagaagaagaagaagaagaagaagaagaagaagaagaagaaga 2404
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 Db 556 ca-cgagcagaagaagaagaagaagaagaagaagaagaagaagaagaagaagaaga 612
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 QY 2405 gta 2408
 ||||
 Db 613 gaga 616

RESULT 8

LOCUS BM087952 572 bp mRNA linear EST 19-NOV-2001
 DEFINITION 501280 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
 ACCESSION BM087952
 VERSION BM087952.1 GI:16948580

KEYWORDS EST.
 SOURCE cow.
 ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovidae; Bovinae; Bos.
 1 (bases 1 to 572)
 Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
 Casas,F., Wray,J.E., White,J., Cho,J., Fahrnenkrug,S.C., Bennett,
 G.L., Heaton,M.P., Lasegred,W.W., Rohrer,G.A., Chiklo-Mckown,C.G.,
 Pertea,G., Holt,I., Katamycherai,S., Liang,F., Quackenbush,J. and
 Keele,J.W.

REFERENCE

AUTHORS

TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA
 libraries and construction of a gene index for cattle
 JOURNAL Genome Res. 11 (4): 626-630 (2001)
 MEDLINE 21180013

COMMENT

Contact: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 P.O. Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smithemall@marc.ars.usda.gov
 Single pass sequencing. Bases called and alt_trimmed with phred
 v0.981004.e. Vector identified by cross-match with the -mnscore 18
 and -mismatch 12 options.
 PCR primers
 FORWARD: AGCAACAGATGATGACCAT
 BACKWARD: GTTTCGACGACGACGACG
 Plate: 149 row: J column: 9
 Seq primer: ATTGAGTGAATGACTATATG.
 location/qualifiers

FEATURES

source

1..572
 /organism="Bos taurus"
 /db_xref="taxon:9913"
 /clone_lib="MARC 2BOV"
 /issue_type="Pooled"
 /lab_host="DH10B"
 /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;"

BASE COUNT 170 a 137 c 125 g 140 t
 ORIGIN
 Library made from pooled tissue from testis, thymus,
 semitendinosus muscle, longissimus muscle, pancreas,
 adrenal, and endometrium."

Query Match 18.6%; Score 500; DB 10; Length 572;
 Best Local Similarity 92.18; P-Val 1.2e-125;
 Matches 527; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 2047 tccgatttaccagaatgacattgaacgtctgtgaagaatctatcaacctgttt 2106
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 Db 1 tccgatttaccagaatgacattgaacgtctgtgaagaatctatcaacctgttt 60
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 QY 2107 tggatctcagaagaatgacattgaacgtctgtgaagaatctatcaacctgttt 2166
 |||||||
 Db 61 tggatctcagaagaatgacattgaacgtctgtgaagaatctatcaacctgttt 120
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 QY 2167 agcagtgag 2226
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 Db 121 agcagtgag 180
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 QY 2227 acagatgag 2286
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 Db 181 acagatgag 240
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 QY 2287 atttgcag 2346
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 Db 241 atttgcag 300
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 QY 2347 cccagcagaagaagaagaagaagaagaagaagaagaagaagaagaagaagaaga 2406
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 Db 301 cccagcagaagaagaagaagaagaagaagaagaagaagaagaagaagaagaaga 360
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 QY 2407 gaaagatttacttgaacatttgaacatttgaacatttgaacatttgaacattt 2466
 |||||||
 Db 361 gaaagatttacttgaacatttgaacatttgaacatttgaacatttgaacattt 420
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 QY 2467 actgagaagaagaagaagaagaagaagaagaagaagaagaagaagaagaaga 2526
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 Db 421 actgagaagaagaagaagaagaagaagaagaagaagaagaagaagaagaaga 480
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 QY 2527 aagtcatttgaacatttgaacatttgaacatttgaacatttgaacattt 2586
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 Db 481 aagtcatttgaacatttgaacatttgaacatttgaacatttgaacattt 540
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 QY 2587 gtaagaatgaatataccaagaatctgtatct 2618
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 Db 541 gtaagaatgaatataccaagaatctgtatct 572
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 RESULT 9
 LOCUS BF931516 507 bp mRNA linear EST 22-JAN-2001
 DEFINITION IL2-NT0202-141200-308-H07 NT0202 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BF931516
 VERSION BF931516.1 GI:12348840
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominini; Homo.
 1 (bases 1 to 507)
 Dias Neto,E., Garcia Correa,R., Verjowski-Almeida,S., Ritonos,M.R.,
 Nagel,M.A., da Silva,W. Jr., Zado,M.A., Bordin,S., Costa,F.P.,
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Balda,G.S., Simpson,D.H.,
 Brunstein,A., deoliveira,P.S., Bucher,P., Jonenevel,C.V., O'Hare
 M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
 Simpson,A.J.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7): 3491-3496 (2000)

Db 240 TGATGACACCTTCAGAAACACCCACCAAGCAAGCAAGTCCATTAACCAAGCTTTGG 299

QY 2387 Tgatttgatccggaatataatgaagatttattcttgatccatcttcggaagatcaaca 2446

Db 300 TAGTCGATATCGGAATAGTGAAGATTTCCTTCGGGTCATATTCAGGCGCATTCACAA 359

QY 2447 Ttccattcagttgacttacttaccagaaggaagcttaccgaagggcccttaccctcta 2506

Db 360 TTGATTAATGACTGCATTACTTGTGAGGAGGAGCTTACCGAGGAGCTTACACTGCCA 419

QY 2507 tctctccagaacttcagaaggaagatcattgctatctatggaagatcagaaacacacag 2566

Db 420 TGGTCAGAGCTTCAGAAAGCAAGCTCATTCATCTGCGGAATTCGCAAGCAGACAG 479

QY 2567 ctgaatttgcagcttacccttgatgaagatgaataatcctgatatctaatgagtg 2626

Db 480 CAGGTTTGAAGCTCATCTTGTGAGAGATGAATTCAGAGATCTGTATCTAGATGAGTG 539

QY 2627 gcatataaataaagccaaagagcctcctaccatccatc 2669

Db 540 GCATTAATAATCAAGCTCAGAGGCTCCTCCTCAGCTTCTTC 582

RESULT 11

AV615075 573 bp mRNA linear EST 28-NOV-2001

LOCUS AV615075 Bos taurus adipocyte cell line Bos taurus cDNA clone

DEFINITION E1AD008H11 5', mRNA sequence.

ACCESSION AV615075

VERSION AV615075.1 GI:9750745

KEYWORDS EST.

SOURCE EST.

ORGANISM Bos taurus

REFERENCE 1 Eukariota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Cetartiodactyla: Ruminantia: Pecora: Bovidae: Bovinae: Bovidae: Bovinae: Bos.

1 (bases 1 to 573)

Takasuga, A., Hirotsune, S., Itoh, R., Uchihara, A., Suzuki, H., Aso, H., and Sugimoto, Y.

TITLE Establishment of a high throughput EST sequencing system using poly(A) tail-removed cDNA libraries and determination of 36,000 bovine ESTs

JOURNAL Nucleic Acids Res. 29 (22), E108 (2001)

MEDLINE 21570554

COMMENT Contact: Yoshikazu Sugimoto

Animal Genetics Division

Shirakawa Institute of Animal Genetics

Osakura, Nishino, Nishi-Shirakawa, Fukushima 961-8061, Japan

Tel: 81-248-25-5641

Fax: 81-248-25-5725

Email: kazusugi@ccocn.ocn.ne.jp

Single pass sequencing.

This clone was obtained from a polyA-deleted cDNA library.

FEATURES

Location/Qualifiers

1..573

/organism="Bos taurus"

/db_xref="taxon:9913"

/clone="E1AD008H11"

/clone_lib="Bos taurus adipocyte cell line"

/cell_type="an adipocyte cell line"

/lab_host="DM10R"

/note="Vector: pGL1; Site_1: SalI; Site_2: NotI; Poly A was deleted from a NotI site"

BASE COUNT 147 a 147 c 100 g 179 t

ORIGIN

Query Match 18.4% Score 493; DB % Length 573;

Best Local Similarity 93.6% Pred. No. 7e-123;

Matches 525; Conservative 0; Mismatches 35; Indels 1; Gaps 1;

QY 1690 gcttgcattatgataatgctgcttatttcccaaatcattataacttctcta 1749

11 ||||||| ||||||| ||||||| ||||||| |||||||

Db 12 GCTCTGCTATGCTGTATGCTGCTTTATGCCCAAMIACTGTATCAACTTCTCTTG 71

QY 1750 aaagacactacatattatatacaagatattt gacttcttctctcaatattacatt 1808

Db 72 AAAGATCACTCATATGAATCAAGATATCAAGATGAGCTGCTGTCTCAATGATTCAT 131

QY 1809 tctatctcaagactgaatataatcattcctcaatagagattgattctcaaatctctatgc 1868

Db 132 TCATGATCCAGACTTAAGCATATCATCTGAATGAGATTGATTATTCAGATCTCTATGC 191

QY 1869 catcccttgatttcttaccatatttactcatatatttccatcaccaaatcttccact 1928

Db 192 CATCCCTTGCTTCTCAACCATGTTTACTGATTAATTCACAGTCAAAAATTTCCAGCT 251

QY 1929 ctgagatacttactacttgaggatctctcttcccatctgactgattgagatgaaatct 1988

Db 252 CTGGGATACCTTACTCTGTGGGAATCTCTCTCCATCTGTATTCGAGATACCAATTC 311

QY 1989 tcaagacactcaggaagccttttgactaatgacttaataatgattctctctctc 2048

Db 312 TCAGCACTCGCTGACCGGACTTTGGTAAATGCTTAATGATGCAATCTCTCTCTC 371

QY 2049 cgatttaccgaatattgacattgaacgctgtgagaagaatctatacaactgtttatg 2108

Db 372 GCACTTACCAAGAAATGACATTGAACGCTGTGCGCAATATCAATCAACTGTTTGTTC 431

QY 2109 gactctcaaaagtactatgacagacatgctgaaccccaaacatctctacag 2168

Db 432 GACTCTAAAGATGCTACTTATAGGAGCATGCTCAACCTCCAAACCAATCTATAG 491

QY 2169 cagtgagagcagaagatctgcagacttattctctgactgagatgacaaatctccaagac 2228

Db 492 CAGTGAGGTAGAGATTCACACCTTATTCCCATGATGATGTCATCTCTCAAAAG 551

QY 2229 agactgtcagaagaatccat 2249

Db 552 AGATCTGTCAAGAGAAATCCAT 572

RESULT 12

BE541855 799 bp mRNA linear EST 09-AUG-2000

LOCUS BE541855

DEFINITION 601064138F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3450752 5', mRNA sequence.

ACCESSION BE541855

VERSION BE541855.1 GI:9770500

KEYWORDS EST.

SOURCE EST.

ORGANISM human

REFERENCE 1 Homo sapiens

Eukariota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo.

1 (bases 1 to 799)

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: rstraus@nih.gov

Tissue Procurement: ATCC

cDNA library preparation: Life Technologies, Inc.

cDNA library Arrayed by: Invitro Genomics, Inc.

DNA sequencing by: Invitro Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the L.M.A.G.E. Consortium/LLNL dt: <http://image.llnl.gov>

Plate: L1A6425 row: k column: 09

High quality sequence stop: 681.

FEATURES

Location/Qualifiers

1..799

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:3450752"

/clone_lib="NIH_MGC_10"

/cell_line="MGC36"

Query Match 18.4% Score 493; DB % Length 573;

Best Local Similarity 93.6% Pred. No. 7e-123;

Matches 525; Conservative 0; Mismatches 35; Indels 1; Gaps 1;

GenCore version 4.5
Copyright (c) 1994 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using SW model

Run on: August 12, 2002, 04:27:02 ; Search time 1257.11 Seconds

(without alignments)
1731.525 Million cell updates/sec

Title: US-09-707-121-1

Perfect score: 2682

Sequence: 1 atgtttccccctgaagacac.....tccacatctctcaaatatga 2682

Scoring table:

Matched: 1797656 seqs, 1046126293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database : GenBank:
1: gb_ba:*
2: gb_ba:*
3: gb_in:*
4: gb_in:*
5: gb_ov:*
6: gb_ov:*
7: gb_ph:*
8: gb_ph:*
9: gb_pr:*
10: gb_pr:*
11: gb_sts:*
12: gb_sts:*
13: gb_ov:*
14: gb_ov:*
15: gb_ba:*
16: gb_ba:*
17: gb_in:*
18: gb_in:*
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26: gb_ov:*
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28: gb_ov:*
29: gb_ov:*
30: gb_ov:*
31: gb_ov:*
32: gb_ov:*
33: gb_ov:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARY

Result No. Query Match length DB ID Description

1	2682	100.0	2682	6	AX140507	AX140507 Sequence
2	2682	100.0	3915	6	AX250162	AX250162 Sequence
3	2659.6	99.2	2679	6	AX099148	AX099148 Sequence
4	2294	85.5	3344	6	BC009208	BC009208 Homo sapi
5	1902	70.9	2152	6	AX356346	AX356346 Sequence
6	865.2	32.3	1422	6	BC020854	BC020854 Homo sapi
7	193	7.2	99878	2	AC087108	AC087108 Homo sapi
8	193	7.2	117217	2	AP002076	AP002076 Homo sapi
9	193	7.2	150339	2	AC093680	AC093680 Homo sapi
10	179.2	6.7	116540	2	AP001957	AP001957 Homo sapi
11	179.2	6.7	121044	2	AC107381	AC107381 Homo sapi
12	178.6	6.7	116530	2	AP001957	AP001957 Homo sapi
13	178.6	6.7	116530	2	AC020749	AC020749 Homo sapi
14	169.8	6.3	135584	2	AC020749	AC020749 Homo sapi
15	156	5.8	9971	2	AC018875	AC018875 Homo sapi
16	156	5.8	319551	2	AE004432	AE004432 Homo sapi
17	145	5.4	17466	2	AC024695	AC024695 Homo sapi
18	137	5.1	72187	2	AC014433	AC014433 Homo sapi
19	120.8	4.5	179248	2	AC106573	AC106573 Homo sapi
20	115.2	4.3	179248	2	AC106573	AC106573 Homo sapi
21	113	4.2	101947	2	AP001820	AP001820 Homo sapi
22	113	4.2	187357	2	AC109361	AC109361 Homo sapi
23	106.6	4.0	64001	2	AC098354	AC098354 Homo sapi
24	106.6	4.0	64001	2	AC098354	AC098354 Homo sapi
25	91.6	3.4	92958	2	U0881117	U0881117 Homo sapi
26	89	3.3	59823	2	U0881117	U0881117 Homo sapi
27	86.6	3.2	156709	2	AX062556	AX062556 Sequence
28	86.6	3.2	156709	2	AC014484	AC014484 Homo sapi
29	84.4	3.1	46463	2	U09830	U09830 Sequence
30	57.2	2.1	7218	6	AF069528	AF069528 Homo sapi
31	55.4	2.1	1459	8	AB062122	AB062122 Mus musc
32	53.4	2.0	2184	10	M05P01	M05P01 Homo sapi
33	53.4	2.0	3313	10	M05P01	M05P01 Homo sapi
34	51.6	1.9	1169	9	BC012622	BC012622 Homo sapi
35	50.6	1.9	523	9	BS022456	BS022456 Homo sapi
36	50.6	1.9	1647	10	RN040819	RN040819 Homo sapi
37	50.6	1.9	1863	9	AB022017	AB022017 Homo sapi
38	50.2	1.9	1808	3	U0881500	U0881500 Homo sapi
39	49.4	1.8	215663	2	AC067717	AC067717 Homo sapi
40	48.4	1.8	2439	8	AF317473	AF317473 Homo sapi
41	48.2	1.8	1453	3	CHRC0866	CHRC0866 Homo sapi
42	48.2	1.8	89724	5	AC093704	AC093704 Homo sapi
43	47.8	1.8	172475	9	AC025613	AC025613 Homo sapi
44	47.4	1.8	1141	6	AX083744	AX083744 Homo sapi
45	47.4	1.8	2219	8	AF144300	AF144300 Candida a

ALIGNMENTS

RESULT 1	AX140507	2682 bp	UWA	11004	PAT 31 MAY 2002
LOCUS	AX140507	Sequence 1 from Patent. W00134783.			
DEFINITION	AX140507				
ACCESSION	AX140507.1	GI:14280626			
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					
	human.				
	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Carnivora; Hominoidea; Homo.				
REFERENCE	1 (bases 1 to 2682)				
AUTHORS	Sands, A.T.				
TITLE	Novel human kinase protein and polynucleotides encoding the same				
JOURNAL	Patent: WO 0134783-A1 17-MAY-2001;				
	Lexicon Genetics Incorporated (US)				
FEATURES					
Source	1..2682				
	/organism "Homo sapiens"				
	/db_xref "taxon:9606"				
BASE COUNT	765 a	576 c	547 g	764 t	
ORIGIN					

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79	100	100	100	0
80	100	100	100	0
81	100	100	100	0
82	100	100	100	0
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99	100	100	100	0
100	100	100	100	0

[illegible]

Dh	928	AGGAGAACCCCAATGAAATTAATGAGAGCAAAAGTATTCAGTGGAGTATCACTTTAT	987
Dy	841	acccccttaccaaacctgccaactgttttcaactctctgagaatgctgcatlaact	900
Dh	988	AGCCGCTTTACCAACCTCCGCACTGGTTTTCATCTTCGCAACAGTCGATTTAACT	1047
Dy	901	ctgcccctgagatcatcattcattgctgtaaaagatataaataatgattacctgacgaaga	960
Dh	1048	CTGCGCTGAGCAATACCTGAGTGTGTAAGAATATATATTAAGATTAAGCTGGCAAGA	1107
Dy	961	ctcatgaagaatgataactcttgatctttgctggaagaagatctggaagaagatctt	1020
Dh	1108	TCATTCAGCAAGGTAATTAATTTGGTGTTGGCTGGAGGTGACTTGGCAAAAGAGCTT	1167
Dy	1021	ctcaacaaagaaatcattcgaatccaaacacccctatctgacactccccaattttctactt	1080
Dh	1168	GTCAACCAAGCAAAATCATTCGATCCAAAGCACTATCTGACACTGCCAATTTCTCTT	1227
Dy	1081	gagagatgataaagctttgagcaagatcagaataaagcttgctctttagatgatacact	1140
Dh	1228	GAGCAATGTAAAGCTTTGCAAAAGCTGCAATAGAACTGCTCTTAAATGATATCACT	1287
Dy	1141	gtgacatgtcgtataacagctaaagaataaataaagaatgtgctggaagaagactt	1200
Dh	1288	GTCAATTGCTGTATGCTAGCTTAAACAATTAATTAAGAATGTGGTGGAAGACATTT	1347
Dy	1201	TACTCAATLaetttaagaaataacactctaacttaccctcattcaaacagcaataatgattg	1260
Dh	1348	TACGATTAAGTTAAATACAGTAGTCAATTAAGCTTCATTCAAACAGTAATATGAGTTC	1407
Dy	1261	ctcgaagctgcaagctcccttcaatcattcagaagaagaagatacagaataccnaactaat	1320
Dh	1408	TCTGCACTGCGACGCTGCTTTATATCACTGAGGAAGAAAGATACAGACTACCAATAAT	1467
Dy	1321	agaatlatctcttcgaacagctgctaaagcttatccgataaaaaaacccaactctg	1380
Dh	1468	ACAATTAATCTCTTGCAAGAGCTGTAAAGCTTATCCATATAAAAAACAATCTGG	1527
Dy	1481	aaagaagcaaatltgaactctcctctataagaatltlaacctgaagctgctctctg	1440
Dh	1528	AAACAAATACAGATTGATATTCCTGCTTATTAAGAGCTTAAAGCTGGGCTGCTTGTG	1587
Dy	1441	gaagtlgaagaaactatcatgccaaatagcatgcaattgataaagaacatccaaactcct	1500
Dh	1588	GAGGTGAGGAGCTATTCATATCCAAATACGATGCAATGTGATAAACACATCCAACTCG	1647
Dy	1501	acataagacaaatltgaagataaatalctctcctgtgcatacgaatagaaatgaaatlatca	1560
Dh	1648	ATCATATACCAATTTAGAGTGAATATTCCTGCTGCATCACTATGAGTGAATCTATCA	1707
Dy	1561	Taccagaagaatcatgcaaaatttaacagatgataaaagcctgaagtagtgcatacct	1620
Dh	1708	TGACCAAGAGTCAATGCAAAATTTAGACGTGTTTAAAGCTGGTGATGTCATCTCT	1767
Dy	1621	gactctgcatltgacaaagatcttaactcaatttatgctccactctctatataaaacttc	1680
Dh	1768	GATCTTGATATGGCAAGGCTTTCATGCTCACTTTCGCTGCATCTCTAATATTAAGCTTC	1827
Dy	1681	aataaagaaccttgccttatgacgataatctgcttatttccaaatccatataaac	1740
Dh	1828	ATAATTAAGGCTTGGCTATGATGATGTGCTGCTTTATATTCACAAATCTGTATAC	1887
Dy	1741	ttctctctaaagaacacagatgataaagaagataatctgaagatctctctcagaag	1800
Dh	1888	TTCTTTTAAAGCAATTCATATGTATATACAAAGCATATGCACTGTCTTCTAGATG	1947
Dy	1801	attgcatltcaatccagaatgaatgaatcaatcgaatgaagattgattlccaaat	1860
Dh	1948	ATTGATTTTCATGCTGACAGCTGAGTAATCATCTCAATGCAATGGTTTATTCAGAT	2007
Dy	1861	ctctatgccatcccttgaattctataagatttactcaatgatalccgaatacgaagaatt	1920
Dh	2008	CTCATGCAATCTTGCTGTTTATACCATCTTATTCATCATGTTTTCACATACCAAAAT	2067

[illegible]

RESULT 9
AC094680/c 150399 bp DNA linear PRI 10-JAN-2002
LOCUS Homo sapiens BAC clone RP11-656C2 from 4, complete sequence.
AC094680
AC094680.2 GI:16259186
VERSION
KEYWORDS
HUGO.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 150399)
Toward a complete human genome sequence
Sullivan, J.F. and Waterston, R.
JOURNAL
genome Res. 8 (11), 1097-1108 (1998)
99063792
2 (bases 1 to 150399)
Rationenko, M., Haylund, K. and Spalding, L.
The sequence of Homo sapiens BAC clone RP11-656C2
JOURNAL
Unpublished (2002)
1 (bases 1 to 150399)
Waterston, R.H.
DIRECT SUBMISSION
Submitted (07-SEP-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 150399)
Waterston, R.H.
DIRECT SUBMISSION
Submitted (03-JAN-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
5 (bases 1 to 150399)
Waterston, R.
DIRECT SUBMISSION
Submitted (10-JAN-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
on Oct 18, 2001 this sequence version replaced g115487523.
COMMENT
Center: Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: <http://genome.wustl.edu/qsc/>
Contact: sapiens@wustl.edu
Summary Statistics
Center project name: H_NH0656C02

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 40); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McNeterson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/qsc>

SOURCE INFORMATION:

The RP11-1 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Moon, P.Y., Zhao, B., Frengen, E., Tatemoto, M., Catalanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome

libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.rscgen.com>) or Pierre de Jong and coworkers at the Roswell Park Cancer Institute (<http://pccpac.med.buffalo.edu>)
VECTOR: pBAC1.6
NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the right is RP13-612N21. Actual start of this clone is at base position 1 of RP11-656C2; actual end is at base position 150399 of RP11-656C2.

FEATURES

SOURCE

Data from AC092458 and AC073229 was used to finish this clone.
AC093680. Polymorphisms have been identified between AC093680.
AC073229 and AC092458.

Location/Qualifiers

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/db_xref="taxon:9606"
/chromosome="4"
/map="4"
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/clone_lib="RP11-1"
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repeat_region
738..893
/rpt_family="MALK"
repeat_region
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repeat_region
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repeat_region
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repeat_region
6202..6471
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repeat_region
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repeat_region
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/rpt_family="L1"
repeat_region
7295..7351
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7354..7393
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repeat_region
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repeat_region
7835..7858
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8242..8541
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8243..8262
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12664..12417
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12421..12541
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repeat_region
12553..12646
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repeat_region
12849..13333
/note="similar to Bos taurus EST B1539025 (NID:q15380145)"
